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ALIGNMENTS

AAB85269 IID AAB8 XX AC AAB8 XX XX DT 07-8 DX Hume XX Hume XX Home XX RESULT 1 Interleukin 20; IL-20; IL-20RA; ZcytoR7; IL-20RB; DIRS1; immunoglobulin; antiinflammatory; antipsoriatic; antiasthmatic; antibacterial; human; 07-SEP-2001 dermatological; Human IL-20 receptor subunit IL-20RA extracellular domain fragment AAB85269 standard; (first antiulcer; protein; entry) antagonist. 221 ₿

WO200146232-A2 Homo sapiens.

28-JUN-2001.

22-DEC-2000; 2000WO-US035307.

23-DEC-1999; 99US-00471774 22-JUN-2000; 2000US-0213416P

(ZYMO) ZYMOGENETICS INC.

Rixon MW, Foster DC, Presnell Xu W, Madden SR, Fox BA; 3 Kelly JD, Sprecher CA, Brandt CS;

WPI; 2001-398320/42.

Isolated interleukin 20 soluble receptor comprising two polypeptide subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus treating inflammatory diseases such as psoriasis.

Claim 1; Page 65; 119pp; English.

The invention relates to an interleukin 20 (II-20) soluble receptor comprising two polypeptide subunits II-20RA (formerly known as ZcytoR7) and II-20RB (formerly known as DIRS1). The two subunits are preferably linked together. In one embodiment, one subunit is fused to the constant region of the light chain of an immunoglobulin, and the other subunit is fused to constant region of the heavy chain of an immunoglobulin. The light chain and the heavy chain are connected via a disulphide bond. The soluble receptor can be used to down-regulate II-20 and thus treat inflammatory diseases such as psoriasis, inflammatory lung injury such as or bronchitis, adult respiratory disease (ARD), septic

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(JASP/)
(CHAN/)
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(SPRE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neutrophil; monocyte; basophil; eosinophil; chemoattractant; psoriasis; periodontal disease; rheumatoid arthritis; idiopathic pulmonary fibrosis; angiogenesis-dependent chronic inflammatory condition; lung cancer; melanoma; inflammatory disease; diabetes; arteriosclerosis; cataract;
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JASPERS S R.
CHANDRASEKHER
NOVAK J E.
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SPRECHER C A.
BLUMBERG H.
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FOSTER D C.
XU W.
MADDEN K L.
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Sequence

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The invention describes a method (I) for treating a mammal afflicted with CC a disease in which an interleukin-20 (II-20) polypeptide plays a role comprising administering antagonist of the II-20 polypeptide to the CC comprising administering antagonist of the II-20 polypeptide to the CC cindividual. An important cytokine in the inflammatory process is CC via chemotaxis and the release of granule enzymes. II-8 binds to receptors on neutrophils, monocytes, basophils, and eosinophils. II-8 is a potent inducer of angiogenesis in several angiogenesis dependent chemoattractant for neutrophils, and the early stages of CC periodontal disease are characterised by the influx of neutrophils. II-8 is an optent inducer of angiogenesis in several angiogenesis-dependent chemoatric productions, including rheumatoid arthritis, CC psoriasis, and idiopathic pulmonary fibrosis. Additionally, II-8 is an CC important source of angiogenic activity in human lung cancer. Also, II-8 cxpression correlates with experimental metastatic activity of some CC expression correlates with experimental metastatic activity of some CC diseases would be to administer an agent that would inhibit II-8. It has CC been shown that II-20 up-regulates II-8. Therefore antagonists to II-20 cliseases in which the II-20 polypeptide plays a role e.g. inflammatory CC diseases including diabetes, arteriosclerosis, cataracts, reperfusion CC diseases inflammatory bowel disease (lacerative colitis), skin disease (psoriasis, cataracts, reperfusion CC inflammatory lung disease (adult respiratory disease (ARD), asthma, CC bronchitis and pneumonia). This sequence represents a human interleukin-CC (III-20) polypeptide used in developing the method of the invention cc (III-20) polypeptide used in developing the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating inflammatory skin and lung diseases using antibodies against interleukins (IL)-20 (which indirectly modulates activation of IL-8), useful for treating e.g. psoriasis, asthma and bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 21-22; 68pp; English.
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AAE23354

standard;

protein;

Human 27-AUG-2002

IL-20RA

mature (first

extracellular protein.

Human; interleukin-19; IL-19; interleukin-20 receptor alpha; IL-20RA; interleukin-20 receptor beta; IL-20RB; inflammation; atherosclerosis; diabetes; reperfusion injury; cancer; infectious meningitis; cataract

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Matches 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method of down-regulating interleukin (IL)-19. The method involves administration of a polypeptide comprised of the extracellular domain of interleukin-20 receptor alpha (IL-20RA) and the extracellular domain of interleukin-20 receptor beta (IL-20RA). The IL-20RA and IL-20RB are heterodimeric receptors that bind to both IL-19 and mda7. The method is useful for down-regulating IL-19, useful for the treatment of inflammation e.g., in diabetes, artherosclerosis, cataracts, reperfusion injury, cancer, infectious meningitis, rheumatoid arthritis, rheumatic fever and systemic lupus erythematosus. The present sequence is human IL-20RA mature extracellular protein
                   inflammation; single chain antibody; interleukin; IL-20; IL-20RA IL-20RB subunit; antiinflammatory; dermatological; antipsoriatic antiarthritic; respiratory; antiasthmatic; antiucer; antibacter;
                                                                                                                                                                                                                                                                                           ADJ83292 standard;
                                                                                                                                     Human
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                                                                             inflammation;
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                                                                                                                                     IL-20RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE
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                                                                                                                               subunit extracellular
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100.0%; Pr
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Pred. No. 3.3
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SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE

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INRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYFFLETQIGPPEVALTTDEK

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Query Match
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Matches 221
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22-JUN-2000;
22-DEC-2000;
                                                                                                                                                                                                                inflammation in a mammal which comprises administering an antibody, antibody fragment or single chain antibody which specifically binds to a receptor of interleukin (IL)-20 comprising an IL-20RA subunit and an IL-20RB subunit. The method of the invention has antiinflammatory, dermatological, antipporiatic, antiarthritic, respiratory, antiasthmatic, antiulcer, antibacterial, immunosuppressive and gastrointestinal applications and may be useful for reducing or treating an inflammation, including an inflammatory skin disease such as psoriasis, eczema, atopic dermatitis and contact dermatities and sease such as psoriasis, end pneumonia, as well as arthritis, septic shock, multiple organ failure, inflammatory bowel disease, ulcerative colitis or Crohn's disease. The current
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson
Blumberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reducing or treating inflammation, e.g. inflammatory lung disease, comprises administering an antibody, antibody fragment or single chain antibody that specifically binds to an interleukin (IL)-20RA subunit o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atopic dermatitis; contact dermatitis; lung;
adult respiratory distress syndrome; arthritis; septic shock; multiple organ failure; bowel;
ulcerative colitis; Crohn's disease; human; receptor;
                                                                                                                                                Sequence
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(XUWW/)
(MADD/)
                                                                                                                                                                                                      sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-APR-2003;
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SPRECHER C A.
BLUMBERG H.
BAGAN M A.
CAGAN B R.
JASPERS S R.
CHANDRASEKHER V
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Jaspers
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                                                                                                                                                                                                                                                                                                                                                                                                                                             novel method of reducing or treating
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                                                                                          Score 1200;
Pred. No. 3
                                                                                                                                                                                                      IL-20RA subunit-related
                                                                       Mismatches
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                                                                                      3.3e-112;
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Novak JE;
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                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of the human soluble interleukin-20 (IL20) receptor alpha subunit. The invention provides a method for the treatment and/or prevention of inflammation, immune system, cardiovascular and haematopoietic disorders and regulation of cellular proliferation by inhibiting the binding of a cytokine (e.g., interleukin-19, interleukin-20 and/or interleukin-24) to its receptor complex, thereby preventing signal transduction. The method uses purified soluble receptor proteins, such as the soluble IL20 receptor alpha subunit. A pharmaceutical composition comprising the polypeptide, or a fusion protein including the polypeptide, is useful for modulating the physiology or development of a cell in vivo, in vitro and/or in situ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating or preventing inflammation, immune system, cardiovascular and hematopoietic disorders, and regulation of cellular proliferation comprises administering proteins inhibiting cytokine signaling, e.g.
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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DB; ACC58076.
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                                                                                                                                                                                                                                                 100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                               Score 1200; DB 6;
Pred. No. 3.3e-112;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor subunit
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                                                                                                                                                                                                                                                                                                 Length
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AAU12265
IID AAU1
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XX Huma
XX Huma
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XX O7-J
PR 01-I
PR 02-I
PR 03-I
PR 03-I
PR 04-I
PR 04-I
PR 03-I
PR 04-I
PR 03-I
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01-DEC-1999
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     GETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200140466-A2
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  GENENTECH
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                                               2000WO-US023522.
2000WO-US023328.
2000WO-US030952.
2000WO-US030873.
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2000WO-US000277
2000WO-US0003565
2000WO-US004341
2000WO-US004342
2000WO-US004314
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2000WO-US005601
2000WO-US005601
2000WO-US005841
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99WO-US031274
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99WO-US030911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
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Smith V,
PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; co adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing polypeptides, and detect the presence of mammalian tumors e.g. lung,
                                                                                                                                                                                                                                                         AAU29222
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                                                                                                                    PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRN
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                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE
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                                                                                                                  polypeptide
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Æ, Goddard
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Tumas
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A, Godowski PJ, Gurney AL, Sh
Tumas D, Watanabe CK, Wood WI,
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Pred. No. 1.2e-111;
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22-AUG-2000;
24-AUG-2000;
08-NOV-2000;
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2000WS-01940499
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2000WS-0194047P
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2000WS-0196690P
2000WS-0196820P
2000WS-0196820P
2000WS-019882P
2000WS-019885P
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2000WS-US013156P
2000WS-US0131516P
2000WS-US01316P
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2000US-0190828P.
2000US-0191007P.
2000US-0191048P.
2000US-0191314P.
2000US-0193655P.
2000US-0193032P.
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2000US-0209832P.
2000WO-US020710.
2000US-00644848.
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KP, Chen J Ģ , Desnoyers Watanabe CK, ŗ Wood WI, Godowski N Ę, Gurney AL,

N-PSDB; 2001-602746/68. AAS46123.

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Novel nucleic acids encoding PRO polypeptides, used to presence of tumors, such as prostate and breast tumors, screen for modulators of the compounds. diagnose the , in mammals the and ç

Claim 11; Fig 398; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the anima and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate animal

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RESULT 8
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ow; horse; sheep; pig; goat; rabbit; ADEPT;
pendent enzyme mediated prodrug therapy.
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factor alpha; chondrocyte c
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Pred. No. 1.2
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23-APR-1998

24-APR-1998

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26-APR-1998

27-MAY-1998

28-MAY-1998

29-APR-1998

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97US-0063870P
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                                                                                                                                                                                                                              Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; extondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervliver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
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18-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein;
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    97US-0059263P
97US-0059266P
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98US-0101471P

98US-0101475P

98US-0101475P

98US-0101738P

98US-0101739P

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98US-0102240P

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XX Human
XX Huma
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Best Local Sim
Matches 221;
                                                                                                                                                       Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cerv. liver; drug screening; transgenic animal; genetic analysis;
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21; Conservative
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98US-0100751P.
98WO-US019330.
98US-0100684P.
98US-0100919P.
98US-0101014P.
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                                                                                                                                              vulnerary;
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Pred. No. 1.2e-111;
; Mismatches 0;
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05-JUN-1998; 09-JUN-1998; 10-JUN-1998; 10-JUN-1998;

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RESULT 13
ABU99665
ID ABU9965
XX ABU996
XX ABU99
XX O9-AL
DT O9-AL
XX Lumou
XX Lumou
XW Humar
XX tumou
XW tissu
XX XX
XX XX
XX XX
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XX YX YX
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16-SEP-1998;
17-SEP-1998;
17-SEP-1998;
17-SEP-1998;
                                          Human;
tumour
tissue
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          US2003040070-A1
                          Homo sapiens.
                                                                                              09-AUG-2003
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98US-0102570P.
98US-0102570P.
98US-0102584P.
98US-01025684P.
                                                  and transmembrane protein; PRO;
factor alpha; chondrocyte cell;
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Pred. No. 1.2e-111;
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tumour; gene therapy;
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RESULT 14
ABU82904
ID ABU82
XX ABU82
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XX THUMAN
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                Human; PRO chromosome
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Similarity 100.0%;
21; Conservative
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                                                                                                                                              standard;
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                                                        polypeptide #199.
             polypeptide; secreted and transmembrane protein; tumour; mapping; gene mapping; cytostatic.
                                                                                      (first
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98US-0086759P-
98US-0088028P-
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RESULT 15
ABO17709
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            (first entry)
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14-SEP-1998;
14-SEP-1998;
16-SEP-1998;
17-SEP-1998;
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12-JUN-1998;
14-JUL-1998;
28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted and transmembrane protein; PRO; antiinflammatory; antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic; antidiabetic; gene therapy; tumour necrosis factor (TNP)-alpha release; TNP-alpha release; cell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; acquired immunodeficiency syndrome; cancer; diabetic complication;
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2001US-00860216.
2001US-0087203.
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2001US-009088342.
2001US-00908779.
2001US-009088342.
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Baker KP, Gerritsen Smith V, Beresini M, n ME, Goddard Stewart TA, Tumas Deforge L, Desnoyers L, Filvaroff E, G A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z; Gao Ξ

2003-341980/32. DB; ACD23946.

N-PSDB; New secreted and transmembrane PRO nucleic acids, for inflammation, organ failure, atherosclerosis, cardiac infertility, birth defecte, premature aging, axquired syndrome (AIDS), or cancer. injury, immunodeficiency treating

Claim 12; Fig 188; 660pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding polypoptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypoptide encoded by (I) is used to detect PRO polypoptides, link a bioactive molecule to a cell expressing a PRO polypoptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF) alpha from human blood, modulate the uptake of glucose or free fatty acid by cells, stimulate or inhibit or which e of, one a to

8888888888888888 Query Match 100.0%; Score 1200; DB 6; Best Local Similarity 100.0%; Pred. No. 1.2e-111; Matches 221; Conservative 0; Mismatches 0; the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood mononuclear cells, inhibit the binding of A-peptide to factor VIIA, or detect the presence of tumour in a mammal. The nucleic diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and Sequence 542 AA; 199 139 181 121 79 61 19 Н PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK 221 SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE 180 INRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEK 120 SISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLE Length 542; Indels 0; Gaps 198 78 60 0;

Search completed: February 25, Job time : 132.743 secs 밁 S 문 S 멍 Ś 문 ş 2005, 02:39:44

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Copyright (c) 1993 - 2005 Compugen Ltd
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SUMMARIES

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hypothetical prote	protein-tyrosine-p	receptor-like tyro	tyrosine kinase Mp	B8R protein - vacc	cytokine receptor	leukocyte antigen-	leukocyte antigen-	frazzled gene prot	hypothetical prote	frazzled gene prot	rig-1 protein - mo	protein-tyrosine-p	B8R 31K protein pr	projectin - fruit	gene B9R protein -

ALIGNMENTS

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A;Gene: GDB:CRFB4; CRF2-4

A;CrOSB-references: GDB:138168; OMIM:123889

A;Map position: 21q; 21q22.1-21q22.2

A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1

C;Keywords: transmembrane protein
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A;Title: A new member of the cytokine receptor gene family maps on chromosome A;Reference number: A47003; MUID:93300510; PMID:8314576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
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A;Residues: 1-123,'D',125-268,'VGRME' <LU2>
A;Cross-references: EMBL:U08988; NID:g571295; PID:g571296
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A; Residues: 1-325 <LUT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, April 1994
A;Reference number: G06935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q08334; GB:Z17227; NID:g393378; PIDN:CAA78933.1; PID:g39337
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Matches
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Best Local Similarity
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  182
                                              180 EPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQS 215
                                                                                                  131 FLAPKIENEYETW---
                                                                                                                                              126 LTAP-----EKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWL 179
                                                                                                                                                                                                  74 CDFSSLSKYGDHT--LRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMR 130
                                                                                                                                                                                                                                                 66 CDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVV 125
                                                                                                                                                                                                                                                                                                     19 GMVPPPENVRMNSVNFKNILQWESPAFAKG-NLTFTAQYLSYR----IFQDKCMNTTLTE 73
                                                                                                                                                                                                                                                                                                                                                                                                     63;
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EPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDET
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                                                                                                  -TMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNL 181
                                                                                                                                                                                                                                                                                                                                                                                                   94;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 243-264 <RE3>
A;Cross:references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1;
A;Accession: 148426
                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 118-125 < RES>
                                                                                                                                                                                                                                                                                                                                                             Gene 148, 343-346, 1994
A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-free
A;Reference number: I48423; MUID:95047447; PMID:7958966
A;Accession: I48423
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A45283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: CRF2-4:isolation of cDNA clones encoding the human and mouse proteins A;Reference number: JC6311; MUID:97199375; PMID:9047351
A;Accession: JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: 25-Mar-1993 #sequence revision 18-Nov-1994 #text change 09-Jul-2004; Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429; JUZe, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992; Title: Behavior of a cloned murine interferon alpha/beta receptor express; Reference number: A45283; MUID:92262522; PMID:1533935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-349 < GIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status:
                                                                                                                                                 Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1;
                                                                                                                                                                             Molecule type: DNA;Residues: 127-224 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTOSS-references: UNIPROT:P33896; GB:M89641; NID:g194111; NOte: sequence extracted from NCBI backbone (NCBIN:102354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 67
                                                                                                                                        Accession: I48425
                                                                                                                                                                                                                       Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Molecule type: mRNA
;Residues: 1-590 <UZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 67; Conserv
    preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.; Uze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-590 <UZE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYDSEVLRNLEPWTTYCIQVQGFLLDQNRTGEWSEFICERTGNDE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPEMQIESLAESLELRFSAPQ-IENEPETW--TLKNIYDSWAYRVQYWKNGTNEKFQVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----FQDHCKRTASTQCDFS-HLSKY-GDYTVRVRAELADEHSEWV-NVTFCPVEDTIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCVSGGL-----PKPANITELSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCVAGWLGGFILVFALGMIPPPEKVRMNSVNFKNILQWEVP-AFPKTNLTFTAQYESYRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 6.3e
35; Mismatches
from GB/EMBL/DDBJ
                                                                                                                                                                                                                       from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.3e-12;
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, NCBIP:102357)
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                                       PID:g510261
                                                                                                                                                 PID:g755811
                                                                                                                                                                                                                                                              PID:g755810
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PEBS Lett. 313, 255-259, 1992

A,Title: Specific antiviral activities of t
A,Reference number: S27387; MUID:93076908;
A,Accession: S27387
                                                                                                                                                                                            A; Accession: S33770
                                                                                                                                                                                                          Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a
A;Reference number: S33770; MUID:93305725;
                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q04790; EMBL:X68443; NID:g431; A;Experimental source: MDBK cells R;Lim, J.K.; Langer, J.A.
                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, FEBS Lett. 313, 255-259, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interferon alpha receptor type 1 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: S27387; S33770
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C;Keywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 473-590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262 A;Accession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: I48429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 426-445 <RE6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: I48428
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A; Residues: 397-424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
A; Residues: 265-3
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene: IFNAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265-375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OHTTTTKCEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNINRTYCDLSAETSDYEHQYYAKYKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKAILVHISPPGQDGNMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIPELLPETTYCLEVKAIHPSLKKHSNYSTVQCIST 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPSAAGGENLKPPENIDVYIIDDNYTLKWSSHGESMG-SVTFSAEYRTKDEAKWLKVPEC
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Pred. No. 9.7e-09
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                                                                                                                                                                                                                                                                                                                                                                                                        the human alpha; PMID:1446745
                                                                                                                                                                                                            bovine alpha
PMID:8318540
                                                                                                                                                                                                                                                                                                                                                                                                                                                              K.E.; Uze,
                                                                                                                                                                                                                                                                                                                                                                   shown
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                                                                                                                                                                                                                                                                                                     PIDN:CAA48484.1; PID:g432
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                                                                                                                                                                                                                              receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                        are determined
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#text_change 09-Jul-2004

Indels Length

39,

8

77

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A;Gene: GDB:IFNAR1; IFNAR; IFRC
A;Cross-references: GDB:12078; OMIM:107450
A;Cross-references: GDB:12078; OMIM:107450
A;Map position: 21q22.1.21q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; C;Keywords: cytokine receptor; glycoprotein; transmembrane protein F;1-21/Domain: transmembrane #status predicted <TRN1>F;437-455/Domain: transmembrane #status predicted <TRN2>F;437-455/Domain: transmembrane #status predicted <TRN2>F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site:
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submitted to the EMBL Data Library, July 1991
A;Description: The structuree of the human in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 60, 225-234, 1990
A;Title: Genetic transfer of a functional human interferon alpha receptor A;Reference number: A32694; MUID:90124632; PMID:2153461
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A32694
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A;Residues: 1-16,'A',18-329,'V',343-557 <LUT>
A;Cross-references: EMBL:X60459; NID:g32671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-557 <UZE>
A;Cross-references: UNIPROT:P17181; GB:J03171; NID:g184645;
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reference number: S17112; Accession: S17112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Date: 22-Jun-1990 #sequence_revision
;Accession: A32694; S17112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: A32694
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Best Local
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    192
                                              179
                                                                                        143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191
                                                                                                                                                                           84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                           h 14.0%; Score 168.5; DB 2;
Similarity 26.4%; Pred. No. 1.9e-06;
51; Conservative 35; Mismatches 88;
                                                                                    VIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--
                                                                                                                                                                                                        RTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSI
                                                                                                                            SVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTW
                                                                                                                                                                      STKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAI
                                                                                                                                                                                                                                                           AGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNIT
                                                                                                                                                                                                                                                                                                   SGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWLEPNTLYCVHVES 191
                                            LEPNILYCVHVES 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-LSPEITYCLKVKA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDKAIILSISPP----GTKDSIMWAMDR--SSFRYSVVIWKNSSSLEERTETVYPEDKIY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QHITSTKCNFSSVELENVFEKIELRIRAEEGNNTSTWYEVEPFVPFLEAQIGPPDVHLEA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPAASGEANLKPENVEIHIIDDNFFLKWN--SSSESVKNVTFSADYQILGTDNWKKLSGC 76
    LSPETTYCLKVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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28.7%;
    204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 186.5; DB 2;
Pred. No. 5.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-Jun-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon alpha/beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                     Length 557;
                                                                                                                                                                                                                                                                                                                                               Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN: AAA52730.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
A49667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RiAquet, M.; Dembic, Z.; Meriii, G.
RiAquet, M.; Dembic, Z.; Meriii, G.
Cell 55, 273-280, 1988
A;Title: Molecular cloning and expression of the human interferon-gamma receptor.
                                                                                                                                                                                                                                                                                                                                                                                 R;HO, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, Proc. Natl. Acad: Sci. U.S.A. 90, 11267-11271, 1993
A;Title: A receptor for interleukin 10 is related to interferon A;Reference number: A49667; MUID:94068585; PMID:8248239
A;Accession: A49667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin-10 receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 6q23-6q24
C; Superfamily: interferon gamma receptor
C; Keywords: cytokine receptor; transmemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interferon gamma receptor precursor - h
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence revision
                                                                                                                                                                                                              C;Superfamily: interl
C;Keywords: cytokine
                                                                                                                                                                                                                                  A;Gene: Illor
C;Superfamily: interleukin-10 receptor ILloR
                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-575 < RES>
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                                                                                                                                                                                                                                                                                 C;Genetics:
                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: Q61727;
                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: IFNGR1; IFNGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P15260; GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g30691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-489 < AGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: A31555
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                                                                                                                              Matches
                                                                                                                                                  Best Local
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 WSQCVTNHTLVLTWLEPNTLYCVHVE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
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                                                                                  8 LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 LPKPANITFLSINMKNVLQW------TPPEGLQGVKVTYTVQYFIYGQK--KWLNKSEC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A49667
LSAETSDYEHQ---YYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISV 124
                                          LPSPSYVWFEARFFQHILHWKPIPN-QSESTYYEVALKQYGNSTWNDIHICRKAQALSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIQC----QLAIPVSSLNSQYCVSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKSISVVLTAPEKWKRNPED-----LPVSMQQIY----SNLKYNVSVLNTKSNRT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPTPTNVTIESYNMNPIVYWEYQIMPQVP-----VFTVEVKNYGVKNSEWID--AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKI-LTQKEDDCD 196
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDB:120688; OMIM:107470
                                                                                                                                                                                                                 receptor
                                                                                                                                                13.2%;
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                                                                                                                          33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 163.5; DB 2;
Pred. No. 4.2e-06;
Pred. No. 4.2e-06;
                                                                                                                                                Score 159; DB 2;
Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                     GB:L12120;
                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
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                                                                                                                                                                                                                                                                                                 NID:g437615; PIDN:AAA16156.1; PID:g43761.
                                                                                                                              100;
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Length 575 Indels

receptors

32;

Gaps

8

84 67

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interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49947
    A;Note:
              A;Cross-references: UNIPROT:Q63953; GB:S69336; NID:g545841; PIDN:AAB30165.1; A;Experimental source: early B-cell line Y16
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                                                         A; Residues: 1-332 < HEM>
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A;Map position: 11q23.3-11q23.3
C;Superfamily: interleukin-10 receptor IL10R
C;Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Immunol. 152, 1821-1829, 1994
A;Title: Expression cloning and characterization of a human IL-10 receptor A;Reference number: I56215; MUID:94165477; PMID:8120391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: IL10R; HIL-10R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q13651; EMBL:U00672; NID:g482802; PIDN:AAA17896.1; PID:g4828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
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                                                                                Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated
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Best Local :
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    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 SLLTSGEVGE-FCVQVKPSVASRSNKGMWSKEEC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                  LVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGFILGKIQLPRPKMAPAND----TYESIFSHFREYEIAIRKVPGNFTFTHKKVKHENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTAVTLDLYHSNGYRARVRAVDGSRHSNWTVT-----NTRFSVDEVTLTVGSVNLEIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQ 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SVVLTAPEKWKRNPEDLPVSMQQIYSNLK-YNVSVLNTKSNRTWSQCVTNHT-- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSAETSDYEHO--YYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPSPPSVWFEAEFFHHILHWTPIPN-QSESTCYEVALLRYGIESWNSISNCSQ-TLSY-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLKAMDGIIYGTIHPPR----PTITPAGDEYEQVFKDLRVYKISIRKFSELKNATKRVKQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLTA-----PEKWKRNPEDLPV--SMQQIYSNLK-YNVSVLNTKSNRTWSQCVTN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETFTLTVPIGVRKFCVKVLPRLESRINKAEWSEEQCLLITTEQ
    extracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.9%;
    from NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 143; DB 2;
Pred. No. 0.00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
    backbone
(NCBIN:145654,
                                                                                                                                                                                                                                                                                                                                                                                                                                       207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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  NCBIP:145656
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                                     PID:g545842
                                                                                                                                                                                                                                                                          type
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A;Molecule type: mRNĀ
A;Residues: 1-94, E; 96-477 <GRA>
A;Residues: 1-94, E; 96-477 <GRA>
A;Residues: 1-94, E; 96-477 <GRA>
A;Cross-references: GB:M26711; NID:g194126; PIDN:AAA37896.1; PID:g309330
A;Hemmi, S.; Peghini, P.; Metzler, M.; Merlin, G.; Demblc, Z.; Aguet, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 9901-9905, 1989
A;Title: Cloning of murine interferon gamma receptor cDNA: expression in A;Reference number: A34508; MUID:90099370; PMID:2532365
A;Accession: A34508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c)species: Mus musculus (house mouse)
C)species: Mus musculus (house mouse)
C)species: Mus musculus (house mouse)
C)spate: 08-Jun-1990 #sequence revision 08-Jun-1990 #text_change 09-Jul-2004
C)Accession: A34368; A35468; A34423; A34508; A36224; I48941
C)Accession: A34368; A35468; A34423; A34508; Moi 148941
C)Accession: A34368; Muthukumaran, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.; Mariano, T.M.;
C.S.; Muthukumaran, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.; Mariano, T.M.;
J. Biol. Chem. 264, 17939-17946, 1989
A;Title: Molecular Characterization of the murine interferon gamma receptor cDNA.
A,Reference number: A34368; MUID:90036866; PMID:2530216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 265, 4064-4071, 1990
A;Title: Affinity purification, peptide analysis, and cDNA sequence of the mouse interf-A;Reference number: A35468; MUID:90154099; PMID:2137461
A;Accession: A35468
A; Molecule type: mRNA
A; Residues: 10-477 < M
                                                           A;Status: preliminary
                                                                                     A; Title: Expression cloning of the murine interferon gamma A; Reference number: A36224; MUID:90083245; PMID:2531896 A; Accession: A36224
                                                                                                                                                                                                                  R; Munro,
                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-94,'E',96-477 <HEM>
A;Cross-references: GB:M28233; NID:g194131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:J05265; NID:g197964; PIDN:AAA39178.1; PID:g309394
R;Gray, P.W.; Leong, S.; Fennie, B.H.; Farrar, M.A.; Pingel, J.T.; Fernandez-Luna, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 8497-8501, 1989
A;Title: Cloning and expression of the CDNA for the murine interferon gamma receptor.
A;Reference number: A34423; MUID:90046824; PMID:2530582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P15261; GB:M25764; NID:g197962; R;Cofano, F.; Moore, S.K.; Tanaka, S.; Yuhki, N.; Landolfo, J. Biol. Chem. 265, 4064-4071, 1990
                                                                                                                                                                          R;Munro, S.; Maniatis, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989
                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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A; Residues: 1-477 < COF>
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A; Residues: 1-477 < KUM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 ISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCV----TNHTLVLT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLVIHFSP-----PFD-
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                                                                                                                                                                                                                                               PIDN:AAA37898.1;
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S.; Appella, E.
                                                                                                                                                                                                                                                   PID:g309331
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Pestka

J.;

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C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence revision 16-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38500; I38501
R;Soh, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel Cell 76, 793-802, 1994
A;Title: Identification and sequence of an accessory factor required for activation A;Reference number: A49946; MUID:94170380; PMID:8124716
A;Accession: I38500
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A;Residues: 1-63,'Q',65-337 <RE2>
A;Cross-references: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-337 <RES>
A;Cross-references: UNIPROT:P38484;
A;Experimental source: clone pSK1
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                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: clone pJS3
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Best Local S
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                                           TTDEKSISVVLTAP------EKWKRNPEDLPVSMQQIYSNLKYN-VSVLNT 159
                                                                                                                                                                            LPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQ-FKYTDSKWFTADIMSIGVNCTQ
                                                                                                                                                                                                                      LPKPANITFLSINMKNVLOWTPPEGLQGVK-VTYTVQYFIYGQKKWLNKS-----ECRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPKPANITFLSINMKNVLQWTPPEGLQGVKVT--YTVQYFIYGQKKWLNKSECRNINRTY
                                                                                                                                INTTYCDLSAETSD----YEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPE-VAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLTAPEKWKRNPEDLPVSMQQ-----
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                                                                                     ITATECDFTAASPSAGFPMDFNVTLRLRÁELGALHSAWVTMPWFQHYRNVTVGÞÞÉNIEV 148
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                                                                                                                                                                                                                                                               11.4%; Score 136.5; DB 2
22.5%; Pred. No. 0.00051;
tive 33; Mismatches 103
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23.6%; Pred. No. 0.0007;
Live 40; Mismatches 98; Inde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: U05875; NID: g463549; PIDN: AAA16955.1; PID: g463
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                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                 102;
-GIQQVKGPFRSNSISLDNL
                                                                                                                                                                                                                                                                 Indels
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A;Map position: 1922-1921
A;Introns: 34/1; 71/2; 138/1; 197/3; 251/1
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester
F;1-32/Domain: signal sequence #status predicted <SIO>
F;1-32/Domain: tissue factor #status experimental <MAT>
F;33-251/Domain: extracellular #status predicted <EXT>
F;35-274/Domain: transmembrane #status predicted <IMM>
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A;Title: Molecular cloning of the cDNA for tissue factor, A;Reference number: A29062; MUID:87244317; PMID:3297348
A;Accession: A29062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A37422; MUID:89000604; PMID:3166978
A;Contents: annotation; disulfide bonds and fatty acid binding site C;Comment: Tissue factor is an integral membrane glycoprotein that (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Expression of tissue factor can be induced in a variety (C;Comment: Express
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Biochemistry 27, 4227-4231, 1988
A;Title: Human tissue factor contains thioester-linked palmitate and stearate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:J02931; NID:g339501; PIDN:AAA61150.1; PID:g339502
A;Note: part of this sequence, including the amino end of the mature protein, R;Scarpati, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.; Flandermeyer, R.R Biochemistry 26, 5234-5238, 1987
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Thromb. Res. 48, 89-99, 1987
A;Title: Cloning and expression of human tissue factor cDNA.
A;Reference number: A47574; MUID:88100453; PMID:3424286
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C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
C;Accession: A43645; A47574; A28320; A29062; A29672; A29008
R;Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
Biochemistry 28, 1755-1762, 1989
A;Tile: Complete sequence of the human tissue factor gene, a highly regula
A;Reference number: A43645; MUID:89247359; PMID:2719931
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A;Residues: 1-259,'A',261-295 <SCA>
A;Cross-references: GB:M16553; NID:g339503; PIDN:AAA61151.1; PID:g339504
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A; Residues: 1-295 < MOR>
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A;Tille: Isolation of cDNA clones coding for human tissue A;Reference number: A94171; MUID:87260946; PMID:3037536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:119895; OMIM:134390
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A; Residues: 1-295 <FIS>
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275-295/Domain: intracellular #status predicted <INT>
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A;Cross-references: UNIPROT:P20352; GB:M26071; NID:g201924; PIDN:AAA40414.1; PID:g201925; R;Ranganathan, G.; Blatti, S.P.; Subramaniam, M.; Fass, D.N.; Maihle, N.J.; Getz, M.J.

J. Biol. Chem. 266, 496-501, 1991

A;Title: Cloning of murine tissue factor and regulation of gene expression by transformi A;Peference number: A39046; MUID:91093171; PMID:1985911

A;Accession: A39046

A;Molecule type: mRNA

A;Residues: 1-25,'I',27-294 <RAN>

A;Cross-references: GB:M57896; GB:J05713; NID:g201926; PIDN:AAA63400.1; PID:g201927

A;Cross-references: GB:M57896; GB:J05713; NID:g201926; PIDN:AAA63400.1; PID:g201927

A;Note: 26-Thr was also found

C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain C;Superfamily: tissue factor

C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane F;1-29/Domain: signal sequence #status predicted <SIG>
F:01-294/Dromain: tissue factor #status predicted <ANTS.
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_chang
C;Accession: A32318; A39046
R;Hartzell, S; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
Mol. Cell. Biol. 9, 2567-2573, 1989
A;Title: A growth factor-responsive gene of murine BALB/c 3T3
A;Reference number: A32318; MUID:89343974; PMID:2761539
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A; Residues: 1-294 < HAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A32318
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                                                                                                                                                                                                                                                                                                                                                                           ;30-294/Product: tissue factor #status predicted <MAT>
;30-251/Domain: extracellular #status predicted <EXT>
;30-251/Domain: transmembrane #status predicted <EXT>
;37-57,69,200/Binding site: carbohydrate (Asn) (Covalent) #status
;37,57,69,218-241/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                              Query Match
Best Local S
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                                                                                                                                                                                                                                  54;
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                                                         CDLSAE-TSDYEHQYYAKVKA----
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CDLTDEIVKDVTWAYEAKVLSVPRRNSVHGDGDQLVIHGEE-PPFTNAPKFLPYRDTNLG
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; Pred. No. 0.0011;
38; Mismatches 7
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Pred. No. 0.00053;
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A;Status: preliminary
A,Molecule type: mRNA
A;Residues: 33-292 <PAN>
A;Cross-references: RMBL:X53521; NID:g1495; PIDN:CAA37597.1; PID:g3980170
A;Cross-references: RMBL:X53521; NID:g1495; PIDN:CAA37597.1; PID:g3980170
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane c;1-32/Domain: signal sequence #status predicted <SIG>
F;1-32/Domain: signal sequence 
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A;Title: Molecular cloning, characterization and expression of cDNA for rabbit brain A;Reference number: 823681; MUID:92081032; PMID:1746002
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C;Accession: JU0441; S23681
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F;79-87,216-239/Disulfide bonds: #status predicted
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Best Local Similarity
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ATTNTNEFLIDVDKGENYCFSVQAVIPSRKKKQRSPESLTECTSREQ
                                                                                      CVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQ 214
                                                                                                                                                                    -----QSFEQVGTKLNVTVQDARTLVRRNGTFLSLRAVFGKDLNYTLYYWRASSTGKKT 197
                                                                                                                                                                                                                                                  VVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKS-----NRT---W-----SQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                           TSDYEHQYYAKVKAIWGTKCS-----KWAESGRFYPFLETQIGPPEVALTTDEKSIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLTWKSTNFKTILEWEP----KSIDHVYTVQ-ISTRLENW--KSKCFLTAETECDLTDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NITELSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCDLSAE-
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                                                                                                                                                                                                                                                                                                                                             VKDVGQTYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNLGQPTI--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPVIQQFEQDGRKLNVVVKDSLTLVRK-----NGTFLTLRQVFGKDLGYIITYRKGSSTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 130; DB 1; Length 292; Pred. No. 0.0015; 9; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (covalent) #status experimental
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        244
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tis

N;Alternate names: coagulation

factor

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A;Experimental source: adrenal gland
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-35,Domain: signal sequence #status predicted <SIG>
F;36-292/Product: tissue factor #status predicted <SIT>
F;36-292/Product: tissue factor #status predicted <SIT>
F;249-271/Domain: extracellular #status predicted <TMAT>
F;272-292/Domain: intracellular #status predicted <TMAT>
F;372-292/Domain: intracellular #status predicted <TMAT>
F;43,153,181/Binding site: carbohydrate (ABM) (covalent) #status predicted
F;81-89,215-238/Disulfide bonds: #status predicted
F;118,124/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;118,124/Binding site: palmitate (Cys) (covalent) #status predicted
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1319
R;Takayenoki, Y: Muta, T.; Miyata, T.; Iwanaga, S.
Blochem. Blophys. Res. Commun. 181, 1145-1150, 1991
A;Title: cDNA and amino acid sequences of bovine tissue factor.
A;Reference number: JQ1319; MUID:92109720; PMID:1764065
A;Accession: JQ1319
Search completed: February 25, 2005, 02:45:37 Job time : 27.5401 secs
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A; Residues: 1-292 < TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:P30931; GB:S74147; NID:g241438; PIDN:AAB20755.1; PID:g24143
                                                                                                                                               200 NTNGFLIDVDKGENYCFHVQAVILSRRVNQKSPESPIKCTSHEK 243
                                                                                                                                                                                                                         171 NHTLVLTWLEPNTLYCVHVESFV------PGPPRRAQPSEK 205
                                                                                                                                                                                                                                                                                              143 ---QSFEQVGTKLNVTVQDARTLVRANSAFLSLRDVFGKDLNYTLYYWKASSTGKKKATT
                                                                                                                                                                                                                                                                                                                                                                    127 TAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKS-----NRT---W------SQCVT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 VKNVRETYLARVLSYPADTSSSTVEPPFTNSPEFTPYLETNLGQPTI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 NITFLSINMKNVLOWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCDLSAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 TSDYEHQYYAKVKAIWGTKCSKWAE----SGRFYPFLETQIGPPEVALITDEKSISVVL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NITWKSTNFKTILEWEP----KPINHVYTVQ-ISPRLGNWKNK--CFYTTNTECDVTDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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                                                                                                 A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
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1080
1 DEVAILPAPQNLSVLSTNMK.....GRYSAPSQTECVEVQGEAIP 203
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geneseqp1980s:*
geneseqp1990s:*
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geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

K.	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	v	8	7	6	ហ	4.	w	N		NO.	Result	
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Abu82604 Human sec	Novel	Abu58014 Human PRO	Human		Human	Human	Human	Human			Aab33440 Human PRO	Membra	Aay41736 Human PRO		Human	Human	2 Human	Aab85271 Human IL-	ription								

45	44	43	42	41	40	9	38	37	36	35	34	ü	32	<u>υ</u>	30	29	28	27	26
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ABG75853	ABU66861	ABU59388	ABU92323	ABU58945	ABU80391	ABO24856	ABO25936	ABU59239	ABU61122	ABU59666	ABU84924	ABU66585	ABU72490	ABU72244	ABU80885	ABU13905	ABO25238	ABU60523	AB017631
Abg75853	Abu66861	Abu59388	Abu92323	Abu58945	Abu80391	Abo24856	Abo25936	Abu59239	Abu61122	Abu59666	Abu84924	Abu66585	Abu72490	Abu72244	Abu80885	Abu13905	Abo25238	Abu60523	Abo17631
Human	Human	Novel	Novel	Human	Human	Human	Human	Human	Human	Novel	Human	Human	Novel	Novel	Human	Human	Novel	Human	Novel
cla	Bec	hum	mud	Bec	Bec	8eC	PRO	вес	PRO	Bec	sec	PRO	mud m	hun	PRO	PRO	hum	860	mud

ALIGNMENTS

Interleukin 20; IL-20; IL-20RA; ZcytoR7; IL-20RB; DIRS1; immunoglobulin; antlinflammatory; antipsoriatic; antiasthmatic; antibacterial; human; 22-DEC-2000; 2000WO-US035307 28-JUN-2001. WO200146232-A2 Homo sapiens. dermatological; Human IL-20 receptor subunit IL-20RB extracellular domain fragment. 07-SEP-2001 AAB85271; AAB85271 standard; protein; (first entry) antiulcer; antagonist. 203 8

23-DEC-1999; 99US-00471774. 22-JUN-2000; 2000US-0213416P. (ZYMO) ZYMOGENETICS INC.

Foster DC, Xu W, Madden Rixon MW, Presnell SR, F n KL, Ka Fox BA; Kelly JD, Sprecher CA, Brandt CS;

WPI; 2001-398320/42.

Isolated interleukin 20 soluble receptor comprising two polypeptide subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus treating inflammatory diseases such as psoriasis.

Claim 1; Page 69; 119pp; English.

The invention relates to an interleukin 20 (II-20) soluble receptor comprising two polypeptide subunits II-20RA (formerly known as ZcytoR7) and II-20RB (formerly known as IRS1). The two subunits are preferably linked together. In one embodiment, one subunit is fused to the constant region of the light chain of an immunoglobulin, and the other subunit is fused to constant region of the heavy chain of an immunoglobulin. The light chain and the heavy chain are connected via a disulphide bond. The soluble receptor can be used to down-regulate II-20 and thus treat inflammatory diseases such as psoriasis, inflammatory lung injury such as asthma or bronchitis, adult respiratory disease (ARD), septic shock,

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RESULT 2
ABG67202
ID ABG6
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ID ABG6
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X
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Best Local S
Matches 203
       Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inflammation; interleukin-20; IL-20; interleukin-8; IL-8; chemokine; neutrophil; monocyte; basophil; eosinophil; chemoattractant; psoriasis; periodontal disease; rheumatoid arthritis; idiopathic pulmonary fibrosis; angiogenesis-dependent chronic inflammatory condition, lung cancer; melanoma; inflammatory disease; diabetes; arteriosclerosis; cataract; reperfusion injury; cancer; meningitis; rheumatic disease; skin disease; idiopathic pulmonary fibrosis; inflammatory bowel disease; psoriasis; inflammatory lung disease; atopic dermatitis; contact dermatitis; inflammatory lung disease; ARD; adult respiratory disease; asthma;
                                                                                                                                                                                                                                                                                                                                       23-DEC-1999;
22-JUN-2000;
                                                                                                                                                                          (KELL/)
                                                                                                                                                                                                                                             (FOST/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-2000; 2000US-00746359
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                                                                                                      (JASP/)
                                                                                                                               (EAGA/)
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                                                                                                                                                                                                                         (MADD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                               MADDEN K L.

KELLY J D.

SERECHER C A.

SERECHER C A.

BLUMBERG H.

BACAN M A.

JASPERS S R.

CHANDRASECHER Y P.

NOVAK J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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FOSTER D
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2000US-0213341P.
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CC receptors on neutrophils, monocytes, basophils, and eosinophils. IL-8 is CC a potent chemoattractant for neutrophils, and the early stages of CC periodontal disease are characterised by the influx of neutrophils. IL-8 is CC is a potent inducer of angiogenesis in several angiogenesis-dependent CC chronic inflammatory conditions, including rheumatoid arthritis, CC psoriasis, and idiopathic pulmonary fibrosis. Additionally, IL-8 is an CC important source of angiogenic activity in human lung cancer. Also, IL-8 cc expression correlates with experimental metastatic activity of some CC expression correlates with experimental metastatic activity of some CC diseases would be to administer an agent that would inhibit IL-8. It has come considered the constant series of the series of the series of the stages. The method is used for treating constant these diseases. The method is used for treating considered the constant correct diseases including diabetes, arteriosclerosis, cataracts, reperfusion CC diseases including diabetes, arteriosclerosis, cataracts, reperfusion CC injury, cancer, meningitis, rheumatic diseases, idiopathic pulmonary concer, meningitis, rheumatic diseases, idiopathic pulmonary concer, meningitis, rheumatic diseases, idiopathic pulmonary confilmanatory bowel disease (ulcerative colitis), skin disease (psoriasis, eczema, atopic dermatitis and contact dermatitis) or an inflammatory lung disease (adult respiratory disease (ARD), asthma, bronchitis and pneumonia). This sequence represents a human interleukin-cc (IL-20) polypeptide used in developing the method of the invention
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a method (I) for treating a mammal afflicted with a disease in which an interleukin-20 (IL-20) polypeptide plays a role comprising administering antagonist of the IL-20 polypeptide to the individual. An important cytokine in the inflammatory process is interleukin-8 (IL-8), a chemokine that acts as an agonist for neutrophils via chemotaxis and the release of granule enzymes. IL-8 binds to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating inflammatory skin and lung diseases using antibodies against interleukins (IL)-20 (which indirectly modulates activation of IL-8), useful for treating e.g. psoriasis, asthma and bronchitis.
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RESULT 3
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Best Local S
Matches 203
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ilarity 100.0%;
Conservative (
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                                        beta variant (V-IL-20RB)
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Pred. No. 5.1e-109;
; Mismatches 0;
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                                         domain.
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Human; interleukin-19; IL-19; interleukin-20 receptor beta; diabetes; reperfusion injury;

IL-20RB; inflammation; cancer; infectious meni

interleukin-20 receptor alpha; IL-20RA;

atherosclerosis;

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RESULT 4
AAE29065
ID AAE2
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AC AAE2
AC AAE2
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AC Huma
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Best Local Simi
Matches 203;
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                         Human
                                                                                                          AAE29065 standard;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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                         IL-22RB protein
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heterodimeric cytokine receptor; interleukin-22R;
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Pred. No. 5.1e-109;
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Human 06-MAY-2004

interleukin receptor IL-20RB

extracellular domain interleukin;

mature protein. IL-20RA subunit;

IL-20;

(first entry)

inflammation; single chain antibody;

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RESULT 5
ADJ83295
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel heterodimeric cytokine receptor which comprises an interleukin-22R (IL-22R; ZcytoRil)) subunit. Receptor sequences are useful for down-regulating IL-20 and treating inflammatory diseases such as psoriasis, adult respiratory disease, multiple organ failure, septic shock, inflammatory lung injury such as bronchitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soluble heterodimeric cytokine receptor useful for down-regulating interleukin-20 and treating inflammatory diseases, such as psoriasis and asthma, comprises an interleukin-22R subunit and a interleukin-20RB
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21-JUN-2001; 2001US-0299865P
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                                                                                                                      ADJ83295 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                       .0%; Score 1080; DB 5; .0%; Pred. No. 5.1e-109; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Foster DC,
                                                                                                                                                                                                 203
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Query Match
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                                                                                                                                                                                                                                                                                                       The invention relates to a novel method of reducing or treating inflammation in a mammal which comprises administering an antibody, antibody fragment or single chain antibody which specifically binds to a receptor of interleukin (II)-20 comprising an IL-20RA subunit and an IL-20RB subunit. The method of the invention has antiinflammatory, dermatological, antipsoriatic, antiarthritic, respiratory, antiasthmatic, applications and may be useful for reducing or treating an inflammatory including an inflammatory skin disease such as psoriasis, eczema, atopic dermatitis and contact dermatitis or an inflammatory lung disease such as adult respiratory distress syndrome, asthma, bronchitis and pneumonia, as well as arthritis, septic shock, multiple organ failure, inflammatory bowel disease, ulcerative colitis or Crohn's disease. The current sequence is that of the human IL-20RB subunit-related protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reducing or treating inflammation, e.g. inflammatory lung disease, comprises administering an antibody, antibody fragment or single chain antibody that specifically binds to an interleukin (IL)-20RA subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thompson
Blumberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprises administering an antibody, antibody that specifically binds to
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22-JUN-2000; 2000US-0213341P.
22-DEC-2000; 2000US-00746359.
                                                                                                                                                                                                                                         Sequence 203
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(SPRE/)
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KELLY J D.

SPRECHER C A.

SPRECHER C A.

BLUMBERG H.

BACAN M A.

DASPERS S R.

CHANDRASEKHER Y A.

NOVAK J E.
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                                          DEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWC
SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG
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                                                                                                                                      100.0%; Score 1080; DB 8; ilarity 100.0%; Pred. No. 5.1e-109; Conservative 0; Mismatches 0;
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Bagan MA,
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irasekher YA,
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Novak JE;
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11-MAR-1998;
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98US-0080333P

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98US-008127195P

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adhesion disorder;
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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood cosgulation disorders, cancers (callular adhesion disorders. They may also be used to raise antibodies. AAZ33381 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                New secreted and transmembrane polypeptides and useful for treating blood coagulation disorders, adhesion disorders.
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N-PSDB; AAZ34190.
                                                                                                                                                                                                                            Claim
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Similarity 100
03; Conservative
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98US-0088030P.
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98US-0088811P.
98US-0088811P.
98US-008881P.
                                                                                                                                                                                                                                                                                                                                                 polypeptide; PRO polypeptide; LDL receptor; TIE ligand; receptor immunoadhesin; gene mapping.
                                                                                                                                                                                                                                                                                                                                                                            protein PRO1114.
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S-0087759P.
S-0088021P.
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S-0088029P.
S-0088030P.
S-0088033P.
S-0088167P.
S-0088127P.
S-0088217P.
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                                                                                                                              The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-072883/06.
N-PSDB; AAZ65011.
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                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                              Membrane-bound proteins and related
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DEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWC
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llarity 100.0%;
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98US-00967791P

98US-0096894P

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Mismatches 0;
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98US-008858P.
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98US-008960P.
98US-0089968P.
98US-0090647P.
98US-0090651P.
98US-0091646P.

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIPVHLETMEPGAAYCVKAQTFV 180
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990S-0123957P
990S-0125775P
990S-012849p
990S-0131445P
990S-01312371P
990S-0132371P
990S-014758P
990S-014758P
990S-0146222P
990S-0146222P
990S-0146222P
990S-0145698
990C-US020111
990C-US020111
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990C-US021090
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02-DEC-1999; 99WO-US028564.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030999.
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US0003565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004341.
                                                                                                                                                                              (GETH ) GENENTECH INC.
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Ashkenazi Kabakoff F f RC, Lu Y, TA, Tumas D, Baker Lu Y, KP, Goddard A, Gurney AL, Heb Pan J, Pennica D, Shelton DL, , Watanabe CK, Wood WI, Yan M; Hebert C, DL, Smith ۲, Henzel Σ

AAC58605

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 33; Fig 54; 309pp; English.

The present invention describes sixty four human PRO proteins which can CC be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for CC proteins, anti-PRO antibodies, agonists and antagonists are useful for CC treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, contecarthritis, juvenile chronic arthritis, spondyloarthropathies, CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogran's CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic contemune, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, CC immune-mediated renal disease, demyclinating diseases of the central and CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune CC represent for the lung, and transplantation associated diseases including CC represent PCR primers and hybridisation probes used in the isolation of CC represent human PRO polynucleotide and protein sequences given in the cCC exemplification of the present invention

Sequence 311 AA;

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           KAIGRYSAFSQTECVEVQGEAIP
                                                               FHLVIELEDLGPQFEFLVAYWRREPGAEEHVXMVRSGGIPVHLETMEPGAAYCVKAQTFV
                                                                                                SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG
                                                                                                              SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG
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                                               FHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIPVHLETMEPGAAYCVKAQTFV
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RESULT 9 AAY44664

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                                                                         The present sequence is interferon receptor (INFR) HKABF92 encoded by CDNA clone HKABF92 (ATCC No. 209746) derived from human keratinocyte cDNA library. INFR-HKABF92 polypeptides are used in the treatment of disorders associated with viral infection, immune dysfunction and proliferative diseases such as cancer, inflammatory disorders, persistent infection, inflammatory bowel disease, arthritis, leukemias, lymphomas, immunosuppression, inflammatory bowel disease, or myelosuppression. The products can also be activates Jaks-STATS signal transduction pathway in a dose-dependent
                                                    Sequence
                                                                                                                                                                                               Claim 17; Fig 1; 98pp; English.
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      Local Sim
                                                                                                                                                                                                                           products
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ducts for
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DB; AAZ49747.
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ilarity 100.0%;
Conservative 0
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59. .77
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.307
                                                                                                                                                                                                                                                                                                                                                                                                                            "Antigenic epitope-bearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Antigenic epitope-bearing peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Antigenic
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      ç,
   Score 1080; DB 3;
Pred. No. 9.8e-109;
; Mismatches 0;
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RESULT 10
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                                                                                Ashkenazi Al
Ferrara N,
Goddard A,
Kljavin IJ,
Stewart TA,
                                                                                                                                                                                                  30-NOV-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
                 target bioa activities.
                        Novel PRO polypeptides and target bioactive molecules
                                                                                                                                                                                                                                                  23-JUN-1999;
26-JUL-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                              21-APR-1999;
28-APR-1999;
14-MAY-1999;
                                                       WPI; 2000-611443/58.
N-PSDB; AAC78547.
                                                                                                                                                                       05-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                           30-DEC-1999;
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                                                                                                                                                                                                                                                                                                          29-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tag; detection; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human
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                                                                               i AJ, Baker KP,
N, Filvaroff E,
A, Godowski PJ,
IJ, Kuo SS, Nap
TA, Tumas D, Wi
                                                                                                                                           GENENTECH INC.
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99US-0130232P

99US-0131445P

99US-0141637P

99US-0141637P

99US-014569B

99US-0162506P

99US-0162506P

99US-0162506P

99WO-US028551

99WO-US028551

99WO-US031243

12000WO-US031274

2000WO-US000277
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99US-0123957P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                              KP, Botstein D, Desnoyers L, Eaton DL;
ER, Fong S, Gao W, Gerber H, Gerritses
PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA,
Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                     polynucleotides used in detection methods, to to specific cells, and to modulate cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence SEQ ID
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                                                                                                         Eaton DL;
Gerritsen ME;
                                                                                          Shelton
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Claim 12; Fig 142; 636pp; English

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RESULT 11
AAY97046
ID AAY977
XX
AC AAY97
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AC AAY97
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TANGC
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Best Local :
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                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                              cytostatic;
virucide; a
                                                                                                                                                                                                                                                                                                                                                                                         TANGO 242; transmembrane; class II; cytokine receptor; chromosome 3q21; cytostatic; cerebroprotective; immunomodulatory; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY97046 standard; protein; 311 AA.
                                WO200039161-A1
                                                                                                                                            Modified-site
                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAIGRYSAFSQTECVEVQGEAIF 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHLVIELEDLGPQFEFLVAYWRREPGAEEHVXMVRSGGIPVHLETMEPGAAYCVKAQTFV
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                                                                                                                                                                                                                                                                                                                                                                            antibacterial; vasotropic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                        /note= "N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                            label=
                                                                                                                     note= "N-linked glycosylation
                                                                                                                                                                                        'label=
                                                                                                                                                                                                                     label=
                                                                                                                                                                                                                                             label= Mature_protein
                                                                                                                                                                                                                                                                               label Signal peptide
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                                                                                                                                                                                 Fibronectin_III_domain
                                                          Cytoplasmic_domain
                                                                                         Transmembrane_domain
                                                                                                                                                                                                                  Extracellular_domain
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Pred. No. 9.8e-109;
; Mismatches 0;
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RESULT 12
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C AAU12
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                                                                                                                                                                                                                                                prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cart ear; proliferation; glucose; free fatty acid; skeletal muscle; ad A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respectively. The proteins, cDNA and their modulators can be used for the treatment of viral and bacterial infection, inflammatory and autoimmune disorders, vascular injury and inhibition of angiogenesis. In particular, TANGO 241 can be used to treat pancreatic disorders and TANGO 242 can be used to treat pancreatic disorders.
  01-DEC-1999;
                                                    01-DEC-2000; 2000WO-US032678
                                                                                                           07-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                Human PRO1114 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU12187 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel transmembrane proteins, designated TANGO 241 and TANGO 242, members of the class II cytokine receptor superfamily. The TANGO 242 genes have been localized to human chromosomes 1p36 and 3q21.
                                                                                                                                                             WO200140466-A2
                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Fig 3; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecules encoding polypeptides designated TANGO 241 and TANGO 242 used for treating e.g. brain and pancreatic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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DB; AAA51871, AA
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  99WO-US028301
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Pred. No. 9.8e-109;
; Mismatches 0;
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2000WC-US006884
2000WC-US007377
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GENENTECH INC.

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Gao

Isolated , secretory and transmembrane other PRO polypeptides, link bioactive polypeptides, and detect the presence communication of the presence of the prese Gerritsen 2001-408281/43. AAS21259 Stewart TA, Beresini M, ME, Goddard Tumas D, Deforge L, Desnoyers L, A, Godowski PJ, Gurney ; Tumas D, Watanabe CK, W e PRO polypeptide used to detect e molecules to cells expressing of mammalian tumors e.g. lung, y AL, She Wood WI, Filvaroff E, Sherwood S detect Σ, PRO

Claim 12; Fig 32; 813pp; English

prostate,

cervical.

ANUI2172-AAU12446 represent novel human secretory and transmembrane PRO CC polypeptides. The PRO polypeptides are useful to detect other PRO CC polypeptides, to modulate biological activities of cells expressing PRO CC polypeptides, and to detect the presence of mammalian lung, colon, CC present, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. Some CC polypeptide expression in a cell sample to that in a control sample. Some CC polypeptide expression in a cell sample to that in a control sample. Some CC polypeptide expression in a cell sample to that in a control sample. Some CC proliferantion of condition of the Proliferation or gene expression in CC pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-CC lymphocytes, the release of a cytokine from peripheral blood monocytes (C PBMCs), or the proliferation of endothelial cells. Some of the PRO CC polypeptides may modulate glucose or free fatty acid uptake by skeletal CC (TIA. The PRO polypeptides can be used in assays to identify molecules crowled in binding interactions. The polynucleotides encoding PRO Some

Example

2

Page

68-69; 119pp;

English.

The invention relates to an interleukin 20 (IL-20) soluble receptor comprising two polypeptide subunits IL-20RA (formerly known as ZcytoR7) and IL-20RB (formerly known as DRRS1). The two subunits are preferably linked together. In one embodiment, one subunit is fused to the constant region of the light chain of an immunoglobulin, and the other subunit is fused to constant region of the heavy chain of an immunoglobulin. The light chain and the heavy chain are connected via a disulphide bond. The soluble receptor can be used to down-regulate IL-20 and thus treat

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RESULT 13
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Best Local S
Matches 203
                                                                                                    Isolated subunits treating
                                                                                                                                                                         Rixon
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22-JUN-2000;
                                                                                                                                                                                  Foster DC,
                                                                                                                                                                                                                                                   22-DEC-2000;
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                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                           Interleukin 20; IL-20; IL-20RA; ZcytoR7; IL-20RB; DIRS1; immunoglobulin;
antiinflammatory; antipsoriatic; antiasthmatic; antibacterial; human;
dermatological; antiulcer; antagonist.
                                                                                                                                                                                                                                                                                                                                                                    Human IL-20 receptor subunit
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                                                                                                                                                                                                      ( OMYZ)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides can be used to
transgenic or knock out anim
                                                                                                                                            2001-398320/42.
DB; AAH22816.
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s IL-20RA and I
g inflammatory
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                                                                                                                                                                       Presnell
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2000US-0213416P.
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                                                                                                                                                                                   Madden
                                                                                                                                                                       SR,
                                                                                                           20 soluble receptor comprising two polypeptide IL-20RB, useful for down-regulating IL-20 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          out animals and
                                                                                                     diseases such as
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                                                                                                                                                                                                                                                                                                                                                                     IL-20RB
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Pred. No. 9.8e-109;
; Mismatches 0;
                                                                                                                                                                                Kelly JD,
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                                                                                                    psoriasis.
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AABOOG 339
ID AABOOG 329
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Best Local S
Matches 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine receptor protein; CG92; antiinflammatory; antimicrobial; immunosuppressive; blood coagulation disorder; antidiabetic; cytostatic; gastrointestinal; acute pancreatitis; glomerulonephritis; gene therapy; severe combined immunodeficiency; SCID; autoimmune disorder; thrombosls; multiple sclerosls; rheumatoid arthritis; Alzheimer's disease; xenograft; graft versus host disease; GYHD; inflammatory bowel disease; haemostatic; endotoxin shock; psoriasis; osteoporosis; hepatitis; vascular; allograft; careficial carefic haematopoietic; vasculitis; lupus; leukaemia; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crohn's
subunit
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                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cytokine receptor protein, CG92.
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                                                                                 WO200123569-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                             /note= "Shows high homology to sensory transducer signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           note=
                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Mature_human_CG92_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= Signal_peptide
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The present sequence is human cytokine receptor protein, designated as CC G992. G992 is a member of the Class II cytokine receptor (CRF2) family, CC which includes R1 and R2 of chains of the II-10 receptor complex, IRM-CC alpha receptor complex, and tissue factor (TF). G992 DNA and proteins are used in the prevention, diagnosis and treatment of diseases associated with inappropriate cytokine receptor expression such as inflammatory complex include complex journal participation. These disorders include complex journal participation. These disorders include complex journal participation, archivitis, vasculitis, vasculitis, lupus, immune complex journal participation, archivitis, archivitis, vasculitis, lupus, creating various immune deficiencies and disorders such as severe combined immunodeficiency (SCID) and autoimmune disorders such as severe combined immunodeficiency (SCID) and autoimmune disorders such as severe combined immunodeficiency (SCID) and autoimmune disorders disorders (e.g., Alzheimer's disease); sarcoidosis; leukaemias (e.g., erythroleukaemia); inflammations such as graft versus host disease (GVHD), inflammatory bowel disease and endotoxin shock; hyperproliferative disorders (e.g., porlasis); cancers (e.g., non-Hodgkin's lymphoma, prostate cancer) and componiesis com
                                                       haematopolesis regulating activity, tissue growth activity, haemostatic and thromolytic activity, receptor/ligand activity and anti-inflammatory activity. CG92 is also used in assays to identify modulators of cytokine receptor expression and their activities
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Sequence
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Matches 203
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                                                 150
                                                               121 FHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIPVHLETMEPGAAYCVKAQTFV
                                                                                                                                                                                                  203;
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                                                                                                  SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG
                                                                                                              SLTEGPECDYTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG
                                                                                                                                                DEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWC
                                                                                                                                                               DEVAILPAPQNLSVLSTNMKHLLMMSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWC
 KAIGRYSAFSQTECVEVQGEAIP
                                                 FHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIPVHLETMEPGAAYCVKAQTFV
                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                Score 1080; DB 4;
Pred. No. 9.8e-109;
; Mismatches 0;
 232
                        203
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AAU04059 standard;

protein;

311

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AAU04059; 23-OCT-2001

(first entry)

Human

interleukin-20 receptor B,

IL-20RB.

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             Matches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents the Human interleukin-20 receptor B, IL-20RB. The invention relates to treating a mammal afflicted with a disease in which an interleukin-20 (IL-20) polypeptide plays a role, involves administering antagonist of IL-20 polypeptide to the individual. The method is useful for treating psoriasis, eczema, atopic dermatitis, contact dermatitis, adult respiratory disease, asthma, bronchitts and pneumonia and is also useful for treating multiple organ failure, inflammatory lung injury, septic shock, bacterial pneumonia, inflammatory bowel disease, rheumatoid arthritis, ulcerative colitis and Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating interleukin-20 induced inflammation in a mammal, such as adult respiratory disease, eczema, psoriasis, contact dermatitis, multiple organ failure and septic shock, involves administering IL-20 antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 62-63; 117pp; English.
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22-JUN-2000;
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Sprecher CA,
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                                                                                                                                                                                            SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAMSILKHPFNRNSTILTRPGWBITKDG
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KAIGRYSAFSQTECVEVQGEAIP 203
                                                                PHLVI ELEDLGPOFEFLVAYWRREPGAEEHVXWVRSGGI PVHLETMEPGAAYCVKAQTFV
                                                                                           FHLVIELEDLGPQFEFLVAYWRREPGAEEHVXMVRSGGIPVHLETMEPGAAYCVKAQTFV
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                                                                                                                                                            SLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITKDG
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                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1080; DB 4; ilarity 100.0%; Pred. No. 9.8e-109; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00470898.
2000US-0213341P.
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Blumberg H,
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l, Bagan
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Jaspers SR,
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210 KAIGRYSAFSQTECVEVQGEAIP 232

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Search completed: February 25, 2005, 02:39:47 Job time : 121.257 secs

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Title:
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1080
1 DEVAILPAPQNLSTIMK.....GRYSAFSQTECVEVQGBAIP 203
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ.	₅	4.	w	N	<u>_</u>	NO.	Result
82.5	82.5	82.5	82.5	82.5	83	83.5	83.5	84	84	ū	85.5	88	89	89.5	101.5	101.5	103	112.5	115	117	122.5	137.5	142	151	158	159.5	162	173	Score	
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1178	1170	716	681	454	968	752	329	915	896	1630	1557	984	489	1427	1118	294	292	575	295	292	578	557	590	560	332	325	349	337	Length	
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VLA-2 protein homo	integrin alpha 2 s	hypothetical prote	probable deoxyribo		cytokine receptor	hypothetical prote	quinolinate synthe	autotaxin precurso	interleukin-3 rece	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine k	interferon gamma r	tumor suppressor -	protein-tyrosine-p	tissue factor prec	tissue factor prec	eukin-10	factor	tissue factor prec	interleukin-10 rec	alpha/	interferon alpha/b	interferon alpha r	interferon gamma r	cytokine receptor	interferon recepto	interferon gamma r	Description	

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I50612 AF0247	T11250 T11053 B96568 S67477	A33998 T30938 T10652	T11483 A82787 JQ1655	S53867 JC5765 A54100 A54849
protein-tyrosine k probable exported	cytochrome-c oxida cytochrome-c oxida cytochrome-c oxida hypothetical prote F420-nonreducing h	<pre>integrin alpha-2 c receptor tyrosine hypothetical prote</pre>	cytochrome-c oxida TonB-dependent rec prolactin receptor	DNA (cytosine)-met inositol polyphosp tumor suppressor p collagen alpha 1(V

ALIGNMENTS

RESULT 2 JC6311 interfer C;Specie C;Date: C;Access R;Gibbs,	D Q 8	B & B &	D 9	Query M Best Lo Matches	RESULT 1 138500 interferon C;Species: C;Date: 16. C;Accession R;Soh, J, Cell 76, J, A;Title: Id A;Reference A;Accession A;Molecule A;Residues: A;Cross-ref A;Experimen A;Molecule A;Residues: A;Cross-ref A;Experimen C;Genetics: C;Keywords:
RESULT 2 JC6311 JC6311 interferon receptor-class II cytokine receptor - mouse C;Species: Mus musculus (house mouse) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: JC6311 R;Gibbs, V.C.; Pennica, D.	IPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEA 201	59 WCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNS 106	1 DEVAILPAPONLSVLSTNMKHLLMWSPVIAPGETVYYSVEYOGEYESLYTSHIWIPSS 58 : : : : : : :	Query Match 16.0%; Score 173; DB 2; Length 337; Best Local Similarity 28.2%; Pred. No. 3e-08; Matches 64; Conservative 31; Mismatches 96; Indels 36; Gaps 11;	RESULT 1 138500 interferon gamma receptor accessory factor-1 precursor - human C;Species: Homo sapiens (man) C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004 C;Accession: 138500; 138501 R;Soh, J; Donnelly, R.J; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S. Cell 76, 793-802, 1994 R;Soh, J: Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S. Cell 76, 193-802, 1994 A;Tille: Identification and sequence of an accessory factor required for activation of A;Reference number: A49946; MUID:94170380; PMID:8124716 A;Recession: 138500 A;Molecule type: mRNA A;Residues: 1-337 <res- 1-63,="" 138501="" 21="" 65-337="" 70',="" <re2-="" a;accession:="" a;cross-references:="" a;experimental="" a;map="" a;residues:="" c;genetics:="" c;keywords:="" clone="" cytokine="" embl:u05875;="" embl:u05877;="" nid:9463549;="" nid:9463551;="" pid:9463'="" pid:946352="" pidn:aaa16955.1;="" pidn:aaa16956.1;="" pjs3="" position:="" receptor<="" source:="" td="" uniprot:p38484;=""></res->

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A;Molecule type: DNA
A;Residues: 1-123,'D',125-268,'VGRME' <LU2>
                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data A; Reference number: G06935 A; Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Lutfalla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-325 < LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene family maps
A;Reference number: A47003; MUID:93300510; PMID:8314576
A;Accession: A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: JC6311; MUID:97199375; PMID:9047351
A;Accession: JC6311
A;Status: preliminary
A;Molecular terms.
                                                                                                                                                                                                                                                                                                       A; Gene: GDB: CRFB4; CRF2-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:138168; OMIM:123889
                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U08988; NID:g571295; PID:g571296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     믕
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-349 < GIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT: Q08334; GB: Z17227; NID: g393378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                    83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                               NTTLTECDFS-SLSKYGDHTLRVRAEFADEHSDWVNITFCPV--DDTIIGPPGMQVEVLA 124
                                                                                                                                  VAILPAPQNLSVLSTNMKHLLMW-SPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AESLELRFSAPOIENEPETWTLKNIYDSWAYRVQYWKN--GTNEKFQVVSPYDSEV-LRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLVIELEDLGPQFE------FLVAYWRREPGAEEHVKMVRSGGIPVHLET 165
   DGFHLVIELEDLGPQFE-
                                                                                                  LGMVPPPENVRMNSVNFKNILQWESPAFAKG----NLTFTAQYLSYR----IFQDKCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEPWITYCIQVQGFLLDQNRTGEWSEPICERTGNDEI
                                                                 LTEGPECDVTDDITATVPYNLRVRATLGSQTSAW-SILKHPFNRNSTILTRPGM--EITK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGMIPPPEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYE-SYRS-FQDH------CKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TASTQCDFS-HLSKYGDYTVRVRAELADEHSEWVNVTFCPV--EDTIIGPPEMQI--ESL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEGPECDVTDDITATVPYNLRVRATLGSQTSAW-SILKHPFNRNSTILTRPGMEITKDGF 121
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                     14.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.0%; Score 162; DB 2; 24.4%; Pred. No. 3.2e-07; tive 37; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                         Library,
                                                                                                                                                                       37;
                                                                                                                                                                                       Score 159.5; DB Pred. No. 5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                        April 1994
                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        GB/EMBL/DDBJ
 FLVAYWRREPGAEEHVKMVRSGGIPVH
                                                                                                                                                                       87;
                                                                                                                                                                                                   2;
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                                                                                                                                                                     Indels
                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAA78933.1;
                                                                                                                                                                   41;
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                                                                                                                                                                   Gaps
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162
                                                                                                    67
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A49947
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A;Status: preliminary; nucleic acid A;Molecule type: mRNA
                                                                         Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a
A;Reference number: S33770, MUID:93305725;
A;Accession: S33770
                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid
A;Molecule type: mRNA
A;Residues: 1-560 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon alpha receptor type 1 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Datesion: S27387; S33770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M. Cell 76, 803-810, 1994
A;Title: A novel member of the interferon receptor family complements functionality A;Reference number: A49947; MUID:94170381; PMID:8124717
A;Accession: A49947
                                                                                                                                                                              R; Lim, J.K.; Langer, J.A.
                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q04790; A;Experimental source: MDBK cells
                                                                                                                                                                                                                                                                                                                                    A;Title: Specific antiviral A;Reference number: S27387; A;Accession: S27387
                                                                                                                                                                                                                                                                                                                                                                                                                   R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, FEBS Lett. 313, 255-259, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q63953; GB:869336; NID:9545841; PIDN:AAB30165.1; A;Experimental source: early B-cell line Y16 A;Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656) C;Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-s (;Species: Mus musculius (house mouse) C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change C;Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-332 < HEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 V--LGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETTANA
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1-421,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLTEGPEC-DVTD---DITA-----TVPYN--LRVRATLGSQTSAWSILKHPFNRNST 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVHLETMEPGAAYCVKAQTFV----KAIGRYSAFSQTECVEVQGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTVGPPKNISVTPGKGSLVIHFSPPFDVFHGATFQYLVHYWEKSETQQEQVEGPFKSNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSFSQLAAPLNPRLHLYNDEQILTWEP--SPSSNDPRPVVYQVEYS-----FIDGSWH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LETMEPGAAYCVKAOTFVKAIGRYSAFSOTECVE-VQGEAIP 203
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423-560
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                                                                                                                                                                                                                                                                                                                                                               activities of the human alpha MUID:93076908; PMID:1446745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 158; DB 2;
Pred. No. 7.1e-07;
                                                 sequence
                                                                                                                                                                                                                                  EMBL: X68443; NID: 9431;
                                                                                                                                                                                                                                                                                                              sequence not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                    bovine alpha
PMID:8318540
                                                 not
                                                   shown
                                                                                                                                                                                                                                                                                                                 shown
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                                                                                                                             interferon
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                                                                                                                                                                                                                                    PIDN:CAA48484.1; PID:g432
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                                                                                                                             receptor
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at

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A; Residues: 243-264 < RE3>
A; Residues: 243-264 < RE3>
A; Cross-references: EMBL:U06239; NII
A; Accession: I4846
A; Status: preliminary; translated fx
A; Molecule type: DNA
A; Residues: 265-375 < RE4>
A; Cross-references: EMBL:U06240; NII
A; Accession: I48477
A; Status: preliminary; translated fx
A; Molecule type: DNA
A; Residues: 397-424 < RE5>
A; Cross-references: EMBL:U06241; NII
A; Accession: I48428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 148, 343-346, 1994
A,Title: Structure of the murine interferon alpha/beta receptor-encoding gene:
A,Reference number: I48423; MUID:95047447; PMID:7958966
A,Accession: 148423
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 118-125 <RES>
A,Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
A,Accession: I48424
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 117-224 <RE2>
A,Residues: 117-224 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Rolecule type: mRNA
A; Rolecule type: mRNA
A; Residues: 1-590 < UZES
A; Cross-references: UNIPROT: P33896; G
A; Cross-reference extracted from NCBI
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C;Date
C;Acces
R;Uze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; A;ACcession: I48425
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C;Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429 R;Uze, G; Lutfalla, G; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 https://doi.org/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.
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                                                                                                                                                                                                                                                             Cross-references: EMBL:U06240; NID:g497108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
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52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPSPENIQINADNQIYVLKW------DYPYENATFQAQWLRAFFKKIPGNHSDKWKQIP
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                                            EMBL: U06241; NID: g497110; PIDN: AAA65006.1; PID: g755812
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24.6%; Pred. No. 6.1e-06;
tive 38; Mismatches 87
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I backbone
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(NCBIN:102354,
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, NCBIP:102357)
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                                                                                                                                                                                                                                                             PID:g510262
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A;Gene: GDB:IFNAR1; IFNAR; IFRC
A;Gross-references: GDB:120078; OMIM:107450
A;Gross-references: GDB:120078; OMIM:107450
A;Gross-references: GDB:120078; OMIM:107450
A;Map position: 21q22.1-21q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein
F;1-21/Domain: transmembrane #status predicted <TRN1>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;537-455/Domain: transmembrane #status predicted <TRN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon alpha/beta receptor precursor - human (15pecies: Homo sapiens (man) (2-Jun-1990 #text_change 0 (15pecies: A2-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 0 (15pecies: A32694; S17112 R,UZe, G.; Lutfalla, G.; Gresser, I. (Cell 60, 225-234, 1990 A);Title: Genetic transfer of a functional human interferon alpha A;Reference number: A32694; MUID:90124632; PMID:2153461
                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, July 1991
A;Description: The structuree of the human interferon alpha/beta receptor gene
A;Reference number: S17112
A;Accession: S17112
                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-16,'A',18-329,'V',343-557 <LUT>
A;Cross-references: EMBL:X60459; NID:g32671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lutfalla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-557 < UZE>
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A;Residues: 426-445 <RE6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P17181; GB:J03171; NID:g184645;
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A; Residues: 473-590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Keywords: cytokine receptor; transmembrane
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     Matches
                                                 Query Match
                                                                                                                                                                                                                                                                                                          Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
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                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVKA-IGRYSAFSQTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVYVNCQDSTCDGLNYE--IIFW--ENTSNTKISMEKDGP-EFTLKNLQPLTVYCVQARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTTHCVFSQDTVYTGTFFLHVQASEGNHTSFWSEEKFIDSQKHILPPPPVITVTAMSDTL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLVIELEDL----GPQFEFLVAYWRREPGAEEHVKMVRSGGIPVHLETMEPGAAYCVKAQT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEIT--KDGF 121
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: U06244; NID: g497114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <RE7>
                            12.7%;
22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.1%; Score 142;
24.9%; Pred. No. 4
  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
                          Score 137.5; DB 2;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 4.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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     74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #text_change 09-Jul-2004
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  Indels
                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:AAA52730.1; PID:g30691
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  65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor into
  Gaps
                                                                                                      carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse
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ce

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Gene 98, 265-269, 1991

A;Title: Conservation of tissue for the second 
                                                                                                                                                                                                                                        NyAlternate names: coagulation factor III C;Species: Oryctolagus cuniculus (domestic C;Date: 30-Sep_1993 #sequence_revision 30-C;Accession: JU0441; S23681
                                                                                                                                                                                                             R;Andrews, B.S.; Rehemtulla,
                                                                                                                                                                                                                                                                                                                                                        tissue factor precursor - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
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A;Cross-references: GDB:330958; OMIM:146933
A;Map position: 11q23.3-11q23.3
C;Superfamily: interleukin-10 receptor IL10R
C;Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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A; Residues: 1-578 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Expression cloning A; Reference number: 156215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, J. Immunol. 152, 1821-1829, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin-10 receptor - hum
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: I56215
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: I56215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PECD-VTDDITATVEYNLRVRATLGSQTSAWSILKHPFNRNSTILT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKIQLPRPKMAPANDTY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----RPGMEITKDGFHLVIELEDLGPQF-EFLVAYWRREPG-----ABEHVKMV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDLTAVTLDLYHSNGYRARVRAVDGSRHSNWTVTNTRFSVDEVTLTVGSVNLEIHNGFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPSPPSVWFEAEFFHHILHWTPIPNQSESTCYEVAL----LRYGIESWNSISNCSQTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFNRNSTILTRPGMEITKDGFHLVI-----ELEDLGPQFEFLVAYWRREPGAEEH 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLTEGPECDVTDDITATVPYN------LRVRATLGSQTSAWS------ILKH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPPPENIEVSVQNQNYVLKW------DYTYANMTFQVQWLHAFLKRNPGNHLY---KWK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
            UNIPROT: P24055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIPROT: Q13651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --GEFCVQVKPSVASRSNKGMWSKEECISL 226
                                                                                                                  ssue factor primary sequence among MUID:91200676; PMID:1840552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUID:94165477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LSDSFHIYIGAPKQSGNTPVIQDYPLIYE--IIFWENTSNAERK 383
                                                                                                                                                                                                       A.; Fowler, B.J.; Edgington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                (domestic rabbit)
vision 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 122.5; DB 
Pred. No. 0.0027; 
3; Mismatches 8
         GB:M55390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL:U00672; NID:g482802; PIDN:AAA17896.1; PID:g482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESIFSHFREYEIAI-RKVPGNFTFTHKKVKHENFSLL
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   NID:g165696; PIDN:AAA63469.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                          #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
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                                                                                                                                                                                                    T.S.; Mackman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X.W.
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                                                                                                                                                three
                                                                                                                                                                                                                                                             09-Jul-2004
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                                                                                                                                                mammalian
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PID:g165697
                                                                                                                                             species.
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-295 < MAC>
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F;250-271/Domain: transmembrane #status predicted <TMM>
F;272-292/Jomain: intracellular #status predicted <INT>
F;471-292/Jomain: intracellular #status predicted <INT>
F;411.114.154,167,182/Binding site: carbohydrate (Asn) (covalent) #status
F;79-87,216-239/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: blood coagulation; glycoprotein; lipoprotein; F;1-32/Domain: signal sequence #status predicted <SIG>F;3-32/Product: tissue factor #status predicted <KNT>F;33-292/Product: extracellular #status predicted <EXT>
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A;Residues: 33-292 <PAW>
A;Cross-references: EMBL:X53521; NID:g1495; PIDN:CAA37597.1; PID:g3980170
C;Comment: Tissue factor is an integral membrane glycoprotein that serves
C;Comment: Expression of tissue factor can be induced in a variety of tissue C;Superfamily: tissue factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: brain
R;Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R
Thromb. Haemost. 66, 315-320, 1991
A;Title: Molecular cloning, characterization and expression
A;Reference number: S23681; MUID:92081032; PMID:1746002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;274/Binding site: palmitate (Cys)
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                                                                                                                                                                                                                        84 ETECDLTDEVVKDVGQTYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNLGQPTI 143
                                                                                                                                                                                                                                                                                                                                                                                     11 NLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHI-----WIPSSWCSLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                          E-ITKDGFHLVIBLED------LGPQFEFLVAYWRREPGAEEHVKMVRS 156
TNTNEFLIDVDKGENYCFSVQAVIPSRKRKQRSPESLTECTSREQGRA
                                                                                                          QSFEQVGTKLNVTVQDARTLVRRNGTFLSLRAVFGKDLNYTLYYWR----
                                                  GGIPVHLETMEPGAAYCVKAQTFVKAIGR--YSAFSQTECV-EVQGEA
                                                                                                                                                                                                                                                                          GPECDVTDDITATV--PYNLRVRATLGSQTSAWSILKHPFNRNS-----TILTRPGM 114
                                                                                                                                                                                                                                                                                                                                NLTWKSTNFKTILEWEP------KSIDH------VYTVQISTRLENW--KSKCFLTA
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Pred. No. 0.0036;
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247
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tissue factor precursor [validated] - human N,Alternate names: coagulation factor III C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change C;Accession: A43645; A47574; A28320; A29662; A29672; A29088 A;Title: Complete sequence of the human tissue factor gene, A;Reference number: A43645; MUID:89247359; PMID:2719931 A;Accession: A43645 R; Mackman, N.; Morrissey, J. Biochemistry 28, 1755-1762, J.H.; Fowler, B.; 1989 Edgington, a highly 09-Jul-2004 regulated

cellular

A;Cross-references: UNIPROT:P13726; (R;Fisher, K.L.; Gorman, C.M.; Vehar, Thromb. Res. 48, 89-99, 1987 GB:J02846; NID:g339505; PIDN:AAA61152.1; G.A.; O'Brien, D.P.; Lawn, R.M. PID:g33950

A; Title: Cloning and expression of human tissue factor cDNA A; Reference number: A47574; MUID:88100453; PMID:3424286

A; Accession: A47574

Α.;

Kraus,

of.

A;Molecule type: mRNA
A;Residues: 1-295 <FIS>
A;Residues: 1-295 <FIS>
A;Residues: 1-295 <FIS>
A;Cross-references: GB:M27436; NID:g339507; PIDN:AAA36734.1; PID:g339508
A;Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K.R.; Guha, A
Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987
A;Title: Isolation of cDNA clones coding for human tissue factor: primary
A;Reference number: A94171; MUID:87260946; PMID:3037536
A;Accession: A28320 factor: primary structure

mRNA

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A; Molecule type: mRNA
A; Residues: 1-259, 'A', 261-295 < $CA>
A; Residues: 1-259, 'A', 261-295 < $CA>
A; Cross-references: GB:M16553; NID:g339503; PIDN:AAA61151.1; PID:g339504
A; Cross-references: GB:M16553; NID:g339503; PIDN:AAA61151.1; PID:g339504
A; Bach, R.; Konigsberg, W.H.; Nemerson, Y.
Blochemistry 27, 4227-4231, 1988
A; Title: Human tissue factor contains thioester-linked palmitate and stearate of A; Reference number: A37422; MUID:89000604; PMID:3166978
A; Contents: annotation; disulfide bonds and fatty acid binding site
C; Comment: Tissue factor is an integral membrane glycoprotein that serves as a C; Comment: Expression of tissue factor can be induced in a variety of tissues b
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A Map position: 1922-1921
C Superfamily: tissue factor
C Keywords: blood cosgulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F;1-32/Domain: signal sequence #status predicted <SIG>
F;3-225/Domain: extracellular #status predicted <TMM'>
F;3-251/Domain: transmembrane #status predicted <TMM'>
F;252-274/Domain: intracellular #status predicted <INT>
F;375-295/Domain: intracellular #status experimental
F;156,169/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;277/Binding site: palmitate (Cys) (covalent) #status experimental
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A49667
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A;Cross references: GB:J02931; NID:g339501; PIDN:AAA61150.1; PID:g339502
A;Note: part of this sequence, including the amino end of the mature protein, was confi.
R;Scarpati, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.; Plandermeyer, R.R.; Siegel,
Biochemistry 26, 5234-5238, 1987
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A;Title: Molecular cloning of the cDNA for tissue factor, A;Reference number: A29062; MUID:87244317; PMID:3297348
R;HO, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 199; A;Title: A receptor for interleukin 10 is related
                                                                                               interleukin-10 receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C;Accession: A49667
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A;Title: Human tissue factor: cDNA sequence and chromosome A;Reference number: A29672; MUID:88050796; PMID:2823875
A;Accession: A29672
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Gene: GDB:F3
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Pakhrai, H.; Edgington, T.S.
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RESULT 12
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A;Accession: A49667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-575 <RES>
A;Cross-references: UNIPROT:Q61727; GB:L12120; NID:94374
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C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C;Comment: Expression of tissue factor can be induced in a variety of tissues by certai
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R; Takayenoki, Y.; Mu
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A;Cross-references: UNIPROT:P30931;
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Keywords: cytokine receptor
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                                                                                                                                                                                                                                                                                                                          NLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHI-----WIPSSWCSLTE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y.; Muta, T.; Miyata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSCOLTTFTLDLYHRSYGYRARVRAVDNSQYSNWTTTETRFTVDEVILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PECDVT----DDITATVPYNLRVRATLGSQTSAWSILKHPFNRNSTILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPSPSYVWPEARFFQHILHWKPIPNQSESTYYEVALK-----OYGNSTWNDIHICRKAQA 80
PVHLETMEPGAAYCVKAQTFV--KAIGRYSAFSQTEC
                                                        EQVGTKLNVTVQDARTLVRANSAFLSLRDVFGKDLNYTLYYWKASSTGKKKATTNTNG--
                                                                                                          TKDGFHLVIELED----
                                                                                                                                                               NTECDVTDEIVKNVRETYLARVLSYPADTSSSTVEPPFTNSPEFTPYLETNLGQPTIQSF 145
                                                                                                                                                                                                                  GPECDVTDDITATVPYNLRVRATLGSQTSAWSILKHPFNRN-----STILTRPGME-I 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPAPONLSVLSTNMKHLLMWSPVIAPGETVYYSVEYOGEYESLYTSHIWIPSSWCSLTEG
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      9.5%;
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                                                                                                                                                                                                                                                                                                                                                                               31;
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                                                                                                                                                                                                                                                                                                                                                                            Score 103; DB
Pred. No. 0.07
31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T.; Iwanaga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:S74147; NID:g241438; PIDN:AAB20755.1; PID:g24143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (covalent) #status

    LGPQFEFLVAYWRREPGAEEHVKMVRSGGI 159

                                                                                                                                                                                                                                                                    ---KPINHVYTVQISPRLGNW--KNKCFYTT
                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (covalent) #status
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--FLIDVDKGENYCFHVQAVILSRRVNQKSPESPIKC

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C;Accession: A49724
R;Matozaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, J. Biol. Chem. 269, 2075-2081, 1994
A;Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase A;Reference number: A49724; MUID:94124561; PMID:8294459
A;Accession: A49724
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A;Note: 26-Thr was also found
C;Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor C;Comment: Expression of tissue factor can be induced in a variety of tissues by certain C;Superfamily: tissue factor
C;Superfamily: tissue factor
C;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane F;10-294/Product: tissue factor #status predicted <SIG>F;30-294/Product: tissue factor #status predicted <MAT>F;30-251/Domain: extracellular #status predicted <EXT>F;30-251/Domain: extracellular #status p
                   A; Molecule type:
                                                                                                                                                                                                                                                                                                                    protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human
N;Alternate names: protein-tyrosine-phosphatase, stomach cancer-associated type
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A;Title: Cloning of murine tissue factor and regulation A;Reference number: A39046; MUID:91093171; PMID:1985911 A;Accession: A39046
A;Molecule type: mRNA
A;Residues: 1-25, /1, 27-294 <RAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;252-274/Domain: transmembrane #status predicted <TMM>
F;37,57,169,200/Binding site: carbohydrate (Asn) (covalent) #status
F;75-83,218-241/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P20352; GB:M26071; NID:G201924; PIDN:AAA40414.1; R;Ranganathan, G.; Blatti, S.P.; Subramaniam, M.; Fass, D.N.; Maihle, N.J.; U. Biol. Chem. 266, 496-501, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ranganathan,
J. Biol. Chem.
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A;Title: A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a protein
A:Reference number: A32318; MUID:89343974; PMID:2761539
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: A32318; A39046
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A; Residues: 1-294 <HAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue factor precursor - mouse N_fAlternate names: coagulation factor
                                                                                                                                                                                                                                                       Species: Homo sapiens (man)
;Date: 03-May-1994 #sequence_revision
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Best Local S
Matches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKMVRSGGIPVHLETMEPGAAYC--VKAQTFVKAIGRYSAFSQTECVE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQPVIQQFEQDGRKLNVVVKDSLTLVRKNGTFLTLRQVFGKDLGYIITYRKGSSTGKKTN
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Pred. No. 0.097;
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Getz, M.J.
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                                                                                                                                                                                                         A; Gene:
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A;Residues: 1-1427 <PIE>
A;Cross-references: UNIPROT:Q91562;
                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Expression of a homologue of the A; Reference number: I51668; MUID: 95113183; A; Accession: I51669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor suppressor - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change C;Accession: I51669
R;Pierceall, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, Dev. Biol. 166, 654-665, 1994
                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
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F;205-289/Domain: fibronectin type III repeat homology <3FNC>
F;296-379/Domain: fibronectin type III repeat homology <3FNC>
F;296-379/Domain: fibronectin type III repeat homology <3FND>
F;385-468/Domain: fibronectin type III repeat homology <3FNE>
F;474-558/Domain: fibronectin type III repeat homology <3FNE>
F;564-658/Domain: fibronectin type III repeat homology <3FNG>
F;567-737/Domain: fibronectin type III repeat homology <3FNG>
F;667-737/Domain: transmembrane #status predicted <TMN>
F;762-778/Domain: intracellular #status predicted <INT>
F;767-1118/Domain: intracellular #status predicted <INT>
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F;35,78,83,107,132,149,172,196,203,286,304,312,329,352,376,383,401,436,439,
F;3527Active site: Cys (phosphocysteine intermediate) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1028/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;28-761/Domain: extracellular #status predicted <EXT>
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A;Cross-references: UNIPR
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: PTPRH; SAP-1
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                                                                                                                                                                                                                                           Genetics
                                                                                                                                        Query Match
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                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ords: carcinogenesis; duplication; glycoprotein; phosphoprotein; Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                         XDCCa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 NRNSTILTRPGMEITKDG-----FHLVIELEDLGPQFEFLVAYW------R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 SLYTSHIWIPSSWCSLTEGPECDVTDDITATVP---YNLRVRATLGSQTS-AWSILKHPF 102
          9
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                                                                                                  Similarity
   PONLSVLSTNMKHL-LMWSPVIAPGETVYYSVEY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                       Conservative
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                                                                                                  Score 89.5;
Pred. No. 9
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Pred. No. 0.53;
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                                                                Mismatches
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omple:	775	155	745	95	685	56
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5, 02:	SLKAFN	CAOTEV		SITKOG	BPSSDW	PSSWC
45:39	775 DSKQRYYSIENLEPSSHYVISLKAFNNA	155 RSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIP 203	:	95 WSILKHPENRNSTILTRPGMBITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMV 154	685 GLEKGSQYSFQVAAMTVNGTGPSSDWYTAETPENDLDESQVPDQPSSLHVRPLTTSIIMS 744	PSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSA 94
		YSAFSC		PTGBTB	ETPENDLDESQVPDQPSSLHVRI	PECDVI
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Result
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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Q6dcu5
Q80ur8
Q7zt05
P17181
Q8wtz2
Q764m7
Q9yhv9
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Q8iyy5 homo
P38484 homo
Q9pvj9 gallu
Q9pvb0 gallu
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Q969j5
Q04790
Q7zt26
Q8c352
Q8c352
Q9uhf4
Q6phb0
Q7zt35
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Q6zvu9
Q63953
Q78ec1
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Q08334
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2 sus scrofa
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homo sapien
yallus gall
gallus gall
lomo sapien
mus musculu
homo sapien
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135 12.6 590 2 Q80UU3 135 12.5 508 2 Q6QIU4 135 12.5 508 2 Q9PVKO 130.5 12.1 244 2 Q8IV66 128 11.9 341 2 Q9YGCB 128 11.9 560 2 Q764WB 126.5 11.7 491 2 Q8IZIB 126.5 11.7 520 2 Q8IZIB 126.5 11.7 521 2 Q8ZMLB 125.5 11.6 338 2 Q8OGGS 123 11.4 209 2 Q8GH7 121.5 11.3 333 2 Q7ZT30 122.5 11.3 578 1 IOR HUMAN 119.5 11.1 336 2 Q8OOEB	12.6 500 2 QQ 12.5 508 2 QQ 12.1 2.4 2 QQ 11.7 491 2 QQ 11.7 521 2 QQ 11.3 33 2 QQ 11.3 578 2 QQ 11.1 336 2 QQ 11.1 336 2 QQ 11.1 336 2 QQ 12.1 11.1 11.1 11.1 11.1 11.1 11.1	45
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Q80073 Q6Q114 Q9PVK0 Q9PVK0 Q81V66 Q9YGCB Q9YGCB Q764M8 Q81Z1B Q81U57 Q81U57 Q82ML8: Q810G2 Q96SH7 Q96SH7 Q96SH7 Q17E130 11TR HUMAN Q810EB	080uj3 06qiu4 05pyk0 08iv66 09ygc8 076iu8 076iu8 076iu8 08iu57 06zml8 080018 096sh7 07zt3 01365) 01365)	ผ
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Broom Wart Chara Body Controls ("Generation and initial analysis of more than 15,000 full-length human	•	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	DOTARGETEY N.H., IOUCIMENT O.W., GLEGHIB. D., DICKBOH M.C.,	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouttard G.G.,	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,	≯	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	Rubin G.M.	Hookins R.F. Jordan H. Moore T. Max S.I. Wang J. Heich F	Alterbiet C.C., Colliss F.G., Register E., Giesimest C.W., Grister G.C.,	Risherer D. Colling G. Wagner t. Chemmen C.M. Schiler G.D.	MEDILINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	TISSUE=Cervix, and Skin;			Genome Res. 13:2265-2270(2003).	high formation and anomals.	e-scare	(2224)	Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,	, Watanabe C., Wieand D., Woods K., Xie MH., Yansura D	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,	Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J	Bacon D., roster D., Grimowski L., Jin Y., Johnson S., Lee J.,	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,	٠;	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;	SEQUENCE FROM N.A. (ISOFORM 1).	[1]		Kukaryota; metazoa; Chordata; Craniata; Vertebrata; Kuteleostomi; Mammalia: Ruthoria: Drimates: Catarrhini: Hominidas: Homo		Name=IL20RB; Synonyms=DIRS1;		recepto	25-CT-2004 (Rel. 45, Last sequence update)	45, Created)	Q6UXIO; Q6P438; Q8TAJ7;	UMAN CHANGE CHANGE CONTROL CON	ri 1

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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This SWI
between
the Eurc
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FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL20:

IL24. The IL22RA1/IL20RB dimer is a receptor for IL20 and IL24.

IL21. The IL22RA1/IL20RB dimer is a receptor for IL20 and IL24.

SUBUNIT: Heterdimer with IL20RA and heterodimer with IL22RA1.

SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (Secor send an email to license@isb-sib.ch).
                      Genew; HGNC:
MIM; 605621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wlodawer A., Zdanov A.;
"Characterization of the recombinant extracellular domains of human interleukin-20 receptors and their complexes with interleukin-19 and interleukin-20.";
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MEDLINB=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
Blumberg H., Conklin D., Xu W.F., Grossmann A., Brender T.,
Carollo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
Prunkard D., Sexson S., Sprecher C., Waggie K., West J.,
Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekher Y.A.,
"Interleukin 20: discovery, receptor identification, and role in
                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT,
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biological functions.";
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PubMed=12351624; DOI=10.1074/jbc.M205114200;
Parrish-Novak J., Xu W., Brender T., Yao L., Jones C., West J
Brandt C., Jelinek L., Madden K., McKernan P.A., Foster D.C.,
Jaspers S., Chandrasekher Y.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dumoutier L., Leemans C., Lejeune D., "STAT activation by IL-19, IL-20 and complexes of two types.";
J. Immunol. 167:3545-3549(2001).
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PubMed=11564763;
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verified
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PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pletnev S., Magracheva E., Kozlov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=14580208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Interleukins 19, 20, and 24 signal through two distinct receptor complexes. Differences in receptor-ligand interactions mediate un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol.
                                                                                                                                                                                                                                                IsoId=Q6UXLO-2; Sequence=VSP_011499, VSP_011500; TISSUB SPECIFICITY: Widely expressed with highest levels and testis. Highly expressed in psoriatic skin. SIMILARITY: Belongs to the type II cytokine family of rec SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                    SMILARALIE CONTROL SWISS-PROT entry is copyright. It is produced through swiss-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no rest European Bioinformatics Institutions as long as its content institutions as long as its content are supported by an
                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative
                                                    AY358305;
BC027449;
BC063696;
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                                                                                                                                                                                                                                                                                                                                                       IsoId=Q6UXL0-1;
                                   HGNC:6004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND LIGAND BINDING,
PARAME DOI=10.1021/bi0354583;
Rozlov S., Tobin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. 13:2819-2824(2004).
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     IPR000282;
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                                                 ; AAQ88672.1; -.
; AAH27449.1; -.
; AAH63696.1; -.
Cytok_receptor_2
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                                                                                                                                                 Usage
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RX MEDILIBE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Staplecton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA RAS.S.A., McEwan P. J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P. J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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CARBOHYD
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TRANSMEM
DOMAIN
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                      MGC34923 protein.
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                        Q8IYY5;
01-MAR-2003
                                                                                                                                                                                              TISSUE=Skin;
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                                                                                                                                                                                                                                                                                                                                                                                                                KAIGRYSAFSQTECVEVQGEAIP
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IPR008957;
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Primates;
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FN_III-like.
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/FTId=VSP 011499.
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N-linked (GlcNAc...)
N-linked (GlcNAc...)
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Pred. No. 8.3e-94;
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Best Local :
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausborg R.L., Peingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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                                                                                                                                                                                                                                                                                                                                            TISSUB-Lung fibroblast,
MEDLINE-94170380; PubMed-8124716; DOI-10.1016/0092-8674(94)90354-9;
Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Wang N.,
Emanuel S.L., Schwartz B., Miki T., Pestka S.;
"Identification and sequence of an accessory factor required for
activation of the human interferon gamma receptor.";
Cell 76:793-802(1994).
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01-OCT-1994 (Rel. 30, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
Interferon-gamma receptor beta chain precursor (Interferon-gamma receptor beta (Rel. 4) (Interferon-gamma transducer-1).
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Homo sapiens (Human)
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Krzywinski M.I., Skalska U.,
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GO:0016020; C:membrane; IEA.
GO:0004896; F:hematopoietin/interferon-class GO:0004896; F:hematopoietin/interferon-class gerPro; IPR000282; Cytok receptor_2.
gerPro; IPR008957; FN_III-like.
pueNCE 147 AA; 16945 MW; 71BAF49274618999 C
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c. Natl. Acad. Sci. U.S.
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D.B., Schnerch
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PROSITE, PS50853; FN3; 2.
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GO; GO:0004906; F:interferon-gamma receptor activity; TAS.
GO; GO:0007166; P:cell surface receptor linked signal trans
GO; GO:0009618; P:response to pathogenic bacteria; TAS.
GO; GO:0009615; P:response to virus; TAS.
InterPro; IPR000282; Cyrok receptor 2.
InterPro; IPR0003861; FN III.
InterPro; IPR008957; FN_III-like.
Pfam; PF00041; fn3: 1
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EMBL; U68755; AAC52066.1; -.
PIR; I38500; I38500.
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H-InvDB; HIX0016076;
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Matches

Similarity

6.7e-08

Indels

36;

Gaps

11;

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RESULT 4
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                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9PVJ9;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99177346; PubMed=10077530;
Reboul J., Gardiner K., Monneron D.,
Reboul J., Gardiner K., Monneron D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            radimeration: (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                      Receptor.
                                                                                                                                                                                                                                                                                                                           GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. ..; GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III.
InterPro; IPR008957; FN III.
                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 9:242-250(1999).
EMBL; AF082667; AAD13679.1; -.
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor gene cluster.";
Genome Res. 9:242-250(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=IFNAR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UL-MAK-2004 (TrEMBLrel. 26, Last annotation update)
Interferon alpha/beta receptor 1 (Fragment).
Namo-TENAD1.
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                               PROSITE;
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                                                                                                                                                                                         σ
                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                               PS50853; FN3; 1.
                                                                                                                                                                                      LPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEY-QGEYESLYT--SHIWIPSSWCSL
QTIATVSDLAPSTLYCVKVQAFSEAYNKSSDFSREECIGTAG
                         GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQG
                                                                                                                                 TEGPECDVTDDITAT-VPYNLRVRATLGSQTSAWS-----
                                                                             LKHPFNRNSTILTRPGMEITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
                                                                                                       ITSMKCNLSSVIKPTSASYYFRVQAMNEYNKSCLSKDVEVDPPVTNEIGPPDVKVDISDV
                                                                                                                                                           LLCPTNVRVFALNMKFYLLWDNHY--NEHVTYTVQYLTGYLKNLYDDYSSKWQKVSGCEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I--SLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I PVHLETMEPGAAYCVKAQTFV----KAIGRYSAFSQTECVEVQGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVGPPENIEVTPGEGSLIIRFSSPFDIADTSTAFFCYYVHYW--EKGGIQQVKGPFRSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TILTRPGMEITKDGFHLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCTQITATEC----DFTAASPSAGFPMDFNVTLRLRAELGALHSAWVTMPWFQH--YRNV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WCSLTEGPECDVTDDITATVP-----YNLRVRATLGSQTSAWSIL---KHPFNRNS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFKYTDSKWFTADIMSIGV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVAILPAPONLSVLSTNMKHLLMWSPVIAPGET--VYYSVEYOGEYESLYTSHIWIPSS
                                                                                                                                                                                                                                                                        442
442 i
                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                              Score 173; DB 2; I
Pred. No. 9.3e-08;
7; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ELEDLGPOFE-FLVAYWRREPGAEEHVK-MVRSGG 158
                                                     GPGNKIMSDLYD
                                                                                                                                                                                                                                                                        839EBE92170609E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uze G., Lutfalla G.;
interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               442
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                                                  FSYQILYWKNSSDNEEEVKMKETK
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442
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RESULT

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Q9YHWO
AC Q9YHWO
AC Q9
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          RESULT 6
Q96A1
ID Q96A
AC Q96A
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Best Local S
Matches 60
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Genome Res. 9:242-250(1999).
EMBL; AF08264; AAD11569.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004996; F:hematopoletin/Interferon-class (D:
GO; GO:0004976; F:receptor activity; IEA.
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR003561; FN III.
InterPro; IPR003597; FN III.
                                                                                                                                                                                                                                                                                                                                                                                                                             Q96A41
Q96A41;
Q96A41;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Soluble cytokine class II receptor, short isoform precursor soluble cytokine class II receptor, short isoform precursor for a company of the cytokine class II cytokine captor of the cytokine c
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Q9YHW0;
01-MAY-1999
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SEQUENCE
SEQUENCE FROM N.A.
TISSUE=Mammary gland;
MEDLINE=21518574; PubMed=11607789; DOI=10.1038/sj.gene.6363786;
                                                                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       Name=CRF2-81; Synonyms=IL-22BP, IL22BP, IL22RA2; ORFNames=UNQ5793;
                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99177346; PubMed=10077530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archosauria; Aves; Neognathae; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interferon alpha/beta receptor 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 ITSMKCNLSSVIKPTSASYYFRVQAMNEYSKSCLSKDVEVDPPVTNEIGPPDVKVDISDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 LICPTNVRVFALNMKFYLLWDNHY--NEHVTYTVQYLTGYLKNLYDDYSSKWQKVSGCEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTIATVSDLAPSTLÝCVKVQAFSEÁYNKSSDFSREECIGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLH-----IKITPPG----GPGNKIMSDLYD----FSYQILYWKNSSDNEEEVKMKETK 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKHPFNRNSTILTRPGMEITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEGPECDVTDDITAT-VPYNLRVRATLGSQTSAWS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                               Primates;
                                                                                                                                                                                                                                                                                                                           Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64055 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.0%;
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Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
Catarrhini; Hominidae
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interferon/interleukin-10
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Genome Res. 13:2265-2270 (2003).
EMBL; AJ313161; CAC85634 1; -.
EMBL; AJ297262; CAC83097.1; -.
EMBL; AY040566; AAK85714.1; -.
EMBL; AY040428; AAK91775.1; -.
EMBL; AY044429; AAK91775.1; -.
EMBL; AY044429; AAK91775.1; -.
EMBL; AY044429; AAK91775.1; -.
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MEDLINE=21366522; PubMed=11481447; DOI=10.1073/pnas.171303198;

Xu W., Presnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,

Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer

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Jelinek L., Storey H., Brender T., Hammond A., Topouzis S.,

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"A soluble class II cytokine receptor, IL-22RA2, is a naturally

occurring IL-22 antagonist.";

Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).
                                                                                                                                                                                                                                      Receptor;
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MEDLINB=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Doud P.
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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Wolk K., A
"A novel,
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Dumoutier L., Lejeune
Submitted (DEC-2000) +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane protein
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                                                                                                                                             Similarity
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004896; F:hematopoietin/interferon-class (D200-domain.
004872; F:receptor activity; IEA.
IFR000252; Cytok receptor_2.
IFR008957; FN_III-like.
Signal.
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Asadullah K., Sabat R.;
soluble homologue of the human IL-10
tial expression in placenta.";
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CDLTSB-TSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLV
                             CDVTDDITATV--PYNLRVRATLGSQTSAWSILKHPFNRNSTILTRPGMEITK-DGFHLV
                                                                             PONLSVLSTNMKHLLMWSPVIA-PGETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPE
                                                             PQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYK-----IYGQRQWKNKEDCWGTQELS
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the EMBL/GenBank/DDBJ
                                                                                                                                                                                           MW;
                                                                                                                            30;
                                                                                                                          Score 164.5; DB
Pred. No. 2.7e-07
0; Mismatches 9
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soluble cytokine class II
isoform.
24A6912BFF75100F CRC64;
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J. Exp. Med. 187:571-578 (1998).

J. FINCTION: Receptor for IL10 and IL22. Serves as a essential for the active IL10 receptor complex ar IL10-induced signal transduction events.
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MEDLINE=9719375; PubMed=9047351; DOI=10.1016/S0378-1119(96)00690-7;
Gibbs V.C., Pennica D.;

"CRF2-4: isolation of cDNA clones encoding the human and mouse
                                                                                                                                                                                                                                                                                                                  modified
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Mammalia; Eutheria;
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Eukaryota; M
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                                                                                                                                                                              InterPro; IPR000282; Cytok
InterPro; IPR008957; FN_III
                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL Enropean Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is ified and this statement is not removed. Usage by and foities requires a license agreement (See http://www.isb-sib.send an email to license@isb-sib.ch).
                                                                                                                                                                                                             GO:0004920;
GO:0005515;
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OCT-2002 (TrEMBLrel. 20, Created)

O1-OCT-2003 (TrEMBLrel. 20, Last sequence update)
Interleukin 10 receptor 2 precursor.
Name=Illorb; Synonyms=1110r2;
Mus musculus (Mouse).
Eukaryota; Metazaa
                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
SEQUENCE
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CARBOHYD
CARBOHYD
SEQUENCE
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Submitted (OCT-2001) to the
EMBL; AF440787; AAL40946.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; JC6311; JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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GG:0004920; F:interleukin-10 receptor
GG:0005515; F:protein binding; IPI.
RT; SM00060; FN3; 2.
SITE; PS50853; FN3; 1.
                          168
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PGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAI
                                                              SLHLRFSAPQIENEPETWTLKNIYDSWAYRVQYWKN--GTNEKFQVVSPYDSEV-LRNLE
                                                                                                            GFHL----VIE
                                                                                                                                                TASTQCDFS-HLSKYGDYTVRVRAELADEHSEWVNVTFCPV--EDTIIGPPEMQIESLAE
                                                                                                                                                                                     TEGPECDVTDDITATVPYNLRVRATLGSQTSAW-SILKHPFNRNSTILTRPGMEITK--D
                                                                                                                                                                                                                                  VAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWCSL
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24.7%;
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he EMBL/GenBank/DDBJ
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Pred. No. 1.2e
0; Mismatches
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Pred. No. 1.2e-06;
0; Mismatches 92
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Sciurognathi; Muridae;
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RESULT 9
I10S_HUMAN
ID I10S_HUMAN
AC Q08334;
  MEDLINE-20469498; PubMed-10875937; DOI=10.1074/jbc.M005304200; A Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J., A Wood W.I., Goddard A.D., Gurney A.L.;
Interleukin (IL)-22, a novel human cytokine that signals through Interferon receptor-related proteins CRF2-4 and IL-22R.";
J. Biol. Chem. 275:3133-31339(2000).
C -- FUNCTION: Receptor for IL10 and IL22. Serves as an accessory cessential for the active IL10 receptor complex and to initiate C -- FUNCTION: Receptor Itransduction events.
C -- SUMCELLULAR LOCATION: Type I membrane protein.
C -- SIMILARITY: Belongs to the type II cytokine family of receptor complex and to initiate complex in the sum of the sum 
                                                             entities re
or send an
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995
01-FEB-1995
25-JAN-2005
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lutfalla G., McInnis M. o. "Structure of the human maighbor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tutfalla G., Gardiner K., Uze G.;
"A new member of the cytokine receptor 21 at less than 35 kb from IFNAR.";
Genomics 16:366-373(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97459974; PubMed=9312047; DOI=10.1093/emboj/16.19.
Kotenko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu
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MEDLINE=96054036; PubMed=7563119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION.
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MEDLINE=93300510; PubMed=8314576;
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Eukaryota; Me
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and functional characterization
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J. 16:5894-5903(1997).
  Z17227;
U08988;
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                                                           requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
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(Rel. 31, Last sequence update)
(Rel. 46, Last annotation update)
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  CAA78933.1;
AAA86872.1;
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Primates;
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4) (Cytokine
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comparison with its
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Best Local
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GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0004920; F:interleukin-10 receptor activity; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0006955; P:immune response; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
GO; GO:0007155; P:signal transduction; TAS.
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR000282; FN_III-like.
InterPro; IPR0001187; Tissue_factor.
Pfam; PF01108; Tissue_fac; I.
Direct protein sequencing; Glycoprotein; Receptor; Signater of the company o
                                                                                                                                                                                                                          Q9BUU4;
01-JUN-2001 (
01-JUN-2001 (
25-OCT-2004 (
Interleukin 1
Name=IL10RB;
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CARBOHYD
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                 Q9BUU4
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                               SEQUENCE FROM N.A. TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAILPAPQNLSVLSTNMKHLLMW-SPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTTLTECDFS-SLSKYGDHTLRVRAEFADEHSDWVNITFCPV--DDTIIGPPGMQVEVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGMVPPPENVRMNSVNFKNILQWESPAFAKG-----NLTFTAQYLSYR-----IFQDKCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVE-VQGEAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSLH----MRFLAPKIENBYBTWTMKNVYNSWTYNVQYWKN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGFHLVIELEDLGPQFE-------
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                                                                                                                                                                                                                                         (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence up
(TrEMBLrel. 28, Last annotation
10 receptor, beta,.
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161
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                                                                                                                                             Chordata;
Primates;
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25.7%;
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FIGHP -> VGRME (in Ref. 2).
Missing (in Ref. 2).
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Extracellular (I
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; 66706C79F8514B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 159.5; DB 1
Pred. No. 1.2e-06;
7; Mismatches 87
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                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity.
                                                                                                                                                                                                                                                                                                           sequence update)
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(Potential)
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                                                                                                                                             Buteleostomi;
; Homo.
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Query Match
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Matches 57
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Uddin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
RA Whiting M., Madan A., Tonchman J.W., Green B.D., Dickeon M.C.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickeon M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Tones S. T. Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phelan M., Farmer A.;
Submitted (AUG-2003) to the EME
EMBL; BC001903; AAH01903.1; -.
EMBL; AY323826; AAP72016.1; -.
EMBL; BT009777; AAP88779.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones S.J., Marra M.A.;
"Generation and initial analysis and mouse cDNA sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ptam; PF01108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR000282; Cytok ecept
InterPro, IPR003961; FN III-
InterPro, IPR008957; FN III-11ke.
InterPro, IPR001187; Tiësue facto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rieder M.J., Carringto
Ahearn M.O., Kuldanek
Nickerson D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JAN-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE
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GO:0004896; F:hematopoietin/interferon-class
GO:0004972; F:receptor activity; IEA.
GO:0007596; P:blood coagulation; IEA.
                                       163
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                                                                                                                                                                                                                                                                                                                                                        Similarity
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                        LETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVE-VQGEAIP
                                                                                                                                                                                                                                                                                         VAILPAPQNLSVLSTNMKHLLMW-SPVIAPGETVYYSVBYQGEYESLYTSHIWIPSSWCS
LRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVP
                                                                                  DSLH---
                                                                                                                                                                 NTTLTECOPS-SLSKYGDHTLRVRAEFADEHSDWVNITFCPV--DDTIIGPPGMQVEVLA
                                                                                                                                                                                                        LTEGPECDVTDDITATVPYNLRVRATLGSQTSAW-SILKHPFNRNSTILTRPGM--BITK 118
                                                                                                                     DGFHLVIELEDLGPQFE-----
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Kuldanek S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue L.
                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                            -MRFLAPKIENEYETWTMKNVYNSWTYNVQYWKN--GTDEKFQITPQYDFEV-
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                                                                                                                                                                                                                                                                                                                                                      14.8%;
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.A., Rajkumar N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moreira
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                                                                                                                                                                                                                                                                                                                                   Score 159.5;
Pred. No. 1.2e
37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                      E470726619AF54C2 CRC64;
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Kelley T.,
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les 87;
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n E.J., Yi Q.,
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Q63953
ID Q6395
AC Q6395
AC Q6395
DT 01-NC
DT 01-NC
DT 25-OC
DT 25-OC
DE Ifagr
GN Name-
OC Bukar
OC Mamma
OX NCBI
RN [1]
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Kacariyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
Ka Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A.,
Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
Kimura K., Yanda K., Wagatsuma M., Murakawa K., Kanebori K.,
Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanebori K.,
Kahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AKI24057; BAC85761.1; -.
GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEB
InterPro; IPR000282; Cytok receptor_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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1-204 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein FL742063.
Homo sapiens (Human).
Eukaryota, Metazna. ~
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI TaxID=10090;
                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Creat
01-NOV-1996 (TrEMBLrel. 01, Last
25-OCT-2004 (TrEMBLrel. 28, Last
Ifngr2 protein (Interferon gamma
                                                                                                                                                                                                                                                                                                                                      Q63953
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TISSUE=Synovial membrane tissue;
Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T.,
Suzuki O., Sasano M., Sano S., Nomura R., Yoshikawa Y.
Matsumoto K., Hirano M., Sano S., Momivama H., Onogawa S
                                                                                                                                                                                                                                                                                                             Q63953;
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57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTTLTECDFS-SLSKYGDHTLRVRAEFADEHSDWVNITFCPV--DDTIIGPPGMQVEVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGMVPPPENVRMNSVNFKNILQWESPAFAEG-----NLTFTAQYLSYR-----IFQDKCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 AA;
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Pred. No. 1.:
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nes 87;
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RC STRAIN-ES-7BL/6; TISSUE-Brain;

RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Hopkins R.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Hishards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hishards S., Worley G.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Hilland D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Hilland D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Hilland D.K., Muzny D.M., Sodergren B.J., Dickson M.C.,

RA Hilland D.K., Muzny D.M., Green E.D., Dickson M.C.,

RA Hilland D.K., Moore R., Schein J.S.,

RA Hopkins P.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

RA Hopkins P.J., Schmerch A., Schein J.E.,

RA Jones S.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005615; C:extracellular space; 7
GO; GO:0016021; C:integral to membrane;
InterPro; IPR000282; CVtok receptor_2.
InterPro; IPR003961; FN_III.
InterPro; IPR008957; FN_III-11ke.
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STRAIN=129Sv/J;
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SMART; SM00060; FN3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50853; FN3; 1.
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MGI:107654; Ifngr2.
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                                                                          ILTRP--GMEITKDGFHLVIELE---DL--GPQFEFLVAYWRREPGAEEHVK-MVRSGGI
                                                                                                                                                                                                                                    SLTEGPEC-DVTD---DITA-----TVPYN--LRVRATLGSQTSAWSILKHPFNRNST
                                                                                                                                                                                                                                                                                                                                                                                                                   DEVAILPAPQNLSVLSTNMKHLLMWSPVIAPGETVYYSVEYQGEYESLYTSHIWIPSSWC
VTVGPPKNISVTPGKGSLVIHFSPPFDVFHGATFQYLVHYWEKSETQQEQVEGPFKSNSI
                                                                                                                                                             RLLE-PNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLE-PFQHYEN
                                                                                                                                                                                                                                                                                                                                    DSFSQLAAPLNPRLHLYNDEQILTWEP--SPSSNDPRPVVYQVEYS-----FIDGSWH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8972742;
hee S., Muthukumaran G., Lembo D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 158; DB 2;
Pred. No. 1.7e-06;
9; Mismatches 94
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Best Local
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05-JUL-2004 (TrEMBLrel. 27, Last sequen
05-JUL-2004 (TrEMBLrel. 27, Last annota
Interferon gamma receptor beta subunit.
                                                                       Bukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III-like.
Pfam; PF00041; fn3; 1.
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MEDLINE=94170381; PubMed=8124717; DOI=10.10

Hemmi S., Bohni R., Stark G., Di Marco F.,

"A novel member of the interferon receptor"
                                        NCBI_TaxID=9606;
                                                                                                                        Homo sapiens (Human)
                                                                                                                                               ORFNames=UNQ5793;
                                                                                                                                                                           IL22RA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q78EC1
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GO:0004896; F:hematopoietin/interferon-class
GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                         193
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PS50853; FN3; 1.
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Last sequence update)
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Pred. No. 1.7e-06;
                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT 15
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                  TISSUE=Placenta;

MEDILINE=21518574; PubMed=11607789; DOI=10.1038/8j.gene.6363786;

Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,

Wolk K., Asadullah K., Sabat R.;

"A novel, soluble homologue of the human IL-10 receptor with

preferential expression in placenta.";

Genes Immun. 2:329-334(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-DUL-2004 (TrEMBLrel. 27, Last sequence update)
501uble cytokine class II receptor, long isoform proceed (Interleukin 22-binding protein CRF2-10L).
Name=CRF2-S1, Synonyms=IL22BP;
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EMBL; AY38937; AAQ89997.1; -.
HSSP; P24055; 1A21.
GQ; GQ:0016020; C:membrane; IEA.
GQ; GO:0004896; F:hematopoletin/interferon-class
InterPro; IPR000282; Cytok receptor 2.
InterPro; IPR008957; FN III-like.
SEQUENCE 262 AA; 30418 MW; B46EEF4DE78ADFDA C
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Kotenko S.V., Izotova I.S., Mirochnitchenko O.V., Dickensheets H., Donnelly R.P., Pestka S.; Telephilickenstification coloning, and characterization of receptor that binds IL-22 and neutralizes its active receptor receptor that binds IL-22 and neutralizes its active receptor receptor
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Mammalia, Eutheria,
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                                                                                                                                                    MEDLINE=21286453; PubMed=11390454;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
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n of a novel
activity.";
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                                                                                                                                                                                                                                                                                                                            Receptor;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                               J. Immunol. 166:7096-7103(2001).

EMBL; AJ313162; CAC85635.1; -.

EMBL; AV040567; AAC85715.1; -.

HSSP; P24055; 1A21.

Genew; HGNC:14901; IL22RA2.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016972; F:membrane; IEA.

GO; GO:00048972; F:membrane; IEA.

InterPro; IPR000282; Cytok_receptor_2.

InterPro; IPR000282; FN_III-11ke.
                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                PQNLSVLSTNMKHLLMWSPVIA-PGETVYYSVEYQGEYE-SLYTSHIWIPSSW------
                                                                                                                                                                                                                                                                                                                                                    signal.
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22 263 soluble cytokine class II receptor, long
isoform.
263 AA; 30550 MW; C96ECEC5D78AC79B CRC64;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 25, 2005, 02:24:39; Search time 117.276 Seconds (without alignments)
964.985 Million cell updates/sec

Title: US-09-745-792A-12
Perfect score: 1200
Sequence: 1 VPCVSGGLPKPANITFLSIN......PSEKQCARTLKDQSSEPKAK 221
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

1612378

1612378 seqs, 512079187 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

,	٠,	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	No.	Result	
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Q90w13	Q9by69	Q9jlu8	P15260	Q28589	Q8wtz2	Q6pkd7	Q9gk86	Q7zt35	P17181	Q7zt22	Q80xz4	Q04790	Q764m8
oncorhynchu	homo sapien	cavia porce	homo sapien	ovis aries	homo sapien	homo sapien	ovis aries	tetraodon n	homo sapien	tetraodon n	mus musculu	bos taurus	sus scrofa

ALIGNMENTS

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RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Kay M., Keenan S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.R.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA Loveland J.E., Lovell J., Martin S., McLaren S.J., McLay K.,
RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
RA McMurray A., Moore M.J.F., Wullikin J.C., Niblett D., Nickerson T.,
RA McMurray A., Moore M.J.F., Wullikin J.C.T., Phillips S., Plumb R.W.,
RA McMurray A., Ramsey Y., Ranby S.A., To.T., Phillips S., Plumb R.W.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA Watt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Wyatt J.C., Young L., Sulston J.E., Dunham I., Rogers J., Beck S.;
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Anantha S., Dickensheets
Donnelly R.P., Kotenko S.
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receptor 1 and IL-10 rece
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J. Biol. Chem.
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PubMed=12351624; DOI=10.1074/jbc.M205114200;

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Brandt C., Jelinek L., Madden K., McKernan P.A., Foster
Jaspers S., Chandrasekher Y.A.;

"Interleukins 19, 20, and 24 signal through two distinct
complexes. Differences in receptor-ligand interactions m
biological functions.";
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MEDLINE-21097717; PubMed=11163236; DDI=10.1016/S0092-8674(01)00187-8;
Blumberg H., Conklin D., Xu W.F., Grossmann A., Brender T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15340161; DOI=10.1110/ps.04682504; Zhang Z., Henzel W.J.; "Signal peptide prediction based on analy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dumoutier L., Leemans C., Lejeune D., Kotenko S.V., Renauld J.-C.; "STAT activation by IL-19, IL-20 and mda-7 through IL-20 receptor complexes of two types."; J., Immunol. 167:3545-3549 (2001).
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Cell 104:9-19(2001).
                                                                                                                                                             PubMed=14764663
                                                                                                                                                                                                  SUBUNIT,
                                                                                                                                                                                                                                                               Biochemistry
                                                                                                                                                                                                                                                                                                interleukin-20 interleukin-20.
                                                                                                                                                                                                                                                                                                                                                                                               Wlodawer A., Zdanov A.;
                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=14580208; DOI=10.1021/bi0354583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT, AND LIGAND BINDING.
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interleukin-20 receptors and their complexes with interleukin-19 and
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                                 Dickensheets H., Du
P., Kotenko S.V.;
als through a novel
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PROSITE; PS50853; FN3; FALSE_NEG.
Alternative splicing; Direct protein sequencing; Glycoprotein;
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EMBL; AY358883; AAQ89242.1;
EMBL; AL135902; CAC38375.1;
HSSP; P13726; 2HFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL19, IL24. The IL20RA/IL10RB dimer is a receptor for IL26. -!- SUBUNIT: Heterodimer with IL20RB and heterodimer with IL11-!- SUBCELLULAR LOCATION: Type I membrane protein (By similar: -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Immunol. 172:2006-2010(2004).
                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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SIMILARITY: Belongs to the type II cytokine family of
SIMILARITY: Contains 2 fibronectin type III domains.
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SSUE SPECIFICITY:
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VPCVSGGLPKPANITFLSINMKNVLQWTPPBGLQGVKVTYTVQYF1YGQKKWLNKSECRN
                         VPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRN
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IPR008957; FN_III-like.
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RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Baito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Baito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Schriml I.M., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml I.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Glasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Marchionni L., McKenzle L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Nagashima T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Navasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Wangner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Miyazaki A., Sakai M., Sasaki D., Shibata K., Shinagawa A.,
RA Mishay E., Hayashizaki Y.,
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C STRAIN=129; TISSUEBreast tumor;

C STRAIN=129; TISSUEBreast tumor;

X MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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X MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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Nature 420:563-573(2002).
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STRAIN=C57BL/6G; TISSUE=Oviduct;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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Mammalia; Eutheria;
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(Rel. 45, Last sequence update)
(Rel. 45, Last annotation update)
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between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK054215; BA
EMBL; BC056628; AA
HSSP; P13726; 2HFT
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InterPro; IPR001187; Tissue_facto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF01108; Tissue_fac; 1.
PROSITE; PS50853; FN3; FALSE_NEG
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                                                                                                                                                                                                                                             y Match
Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBCELLULAR LOCATION:
SIMILARITY: Belongs to
SIMILARITY: Contains 2
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SUBUNIT: He
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FUNCTION: The IL20RA/IL20RB dimer is a receptor for IL24. The IL20RA/IL10RB dimer is a receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse cDNA sequences.";
      181
                                                                      121
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PNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK
                                                          SISVVLTAPEK#KRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRT#SQCVTNHTLVLT#LE
                                                                                                                     INRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWABSGRFYPFLETQIGPPEVALTTDEK
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                                          SISIALTAPEKWKRNPQDHT
                                                                                                     INRTYCOLSVETSDYEHQFYAKVKAIWEARCSEWAETERFYPFLETQVSPPEVALTTGEK
                                                                                                                                                                 VPCVFCGLPKPTNITFLSINMKNVLHWNPPESLHGVEVTYTVQYFIYGQKKWLNASKCGS
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AAH56628.1;
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79.6%;
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Potential.
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Fibronectin type-III 2
Fibronectin type-III 2
By similarity.
By similarity.
N-linked (GlCNAc...)
                                                                                                                                                                                                                           Score 965; DB
Pred. No. 1.4e
15; Mismatches
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Cytoplasmic (Potential)
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Extracellular (Potential)
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Q96A41;
Q96A41;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 27, Last annotation update)
Q5-UIL-2004 (TrEMBLrel. 27, Last annotation update)
Soluble cytokine class II receptor, short isoform precursor
(Interleukin 22-binding protein CRF2-10) (Class II cytokine
                                    TISSUE-Mammary gland;
TISSUE-Mammary gland;
MEDLINE=21518574; PubMed=11607789; DOI=10.
Gruenberg B.H., Schoenemeyer A., Weiss B.,
Wolk K., Asadullah K., Sabat R.;
"A novel, soluble homologue of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q96SH7;
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01-DEC-2001
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Genes Immun.
[2]
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SEQUENCE
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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GO:0004895; F:hematopoietin/interferon-class
GO:0004872; F:receptor activity; IEA.
erPro; IPR000282; Cytok receptor 2.
erPro; IPR008957; FN_III-like.
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(TrEMBLrel. 19,
(TrEMBLrel. 25,
(Interleukin 20
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                                2:329-334(2001)
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, Last sequence update)

, Last annotation update)

, receptor alpha, isoform 3
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                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae,
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Catarrhini;
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eiss B., Toschi
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                                                                                                                                                .gene.6363786;
L., Kunz S.,
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EMBL; AJ313161; CAC85634.1; -.

EMBL; AJ297262; CAC83097.1; -.
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"A soluble class II cytokine receptor, IL-22RA2, is a naturally occurring IL-22 antagonist.";
Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22887299; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., I Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S. Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
SIGNAL
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Submitted (DEC-2000)
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GO; GO:0004896; F:hematopoletin/interferon-class
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR008957; FN_III-like.
Decentor. circal
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                                                   NLPYRYQKEKNVSIEDYY-ELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV
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VESFVPGPPRRAQPSEKQC
                                                                                                         EKWKRNPEDLPVSMOQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVH
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C-2000) to the EMBL/GenBank/DDBJ
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3; Mismatches 90
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Schlutsmeyer
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Q800G1;
01-JUN-2003
                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updathelical cytokine receptor CRFB8.
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BMC Genomics 4:29-29(2003).

EMBL; AJ544894; CAB67782.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004896; F:hematopoietin/interferon-class

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR0008957; FN_III-like.
                         Name=crfb8;
Tetracdon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata;
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Acanthomorpha; Acanthopterygii; Percomor
Tetradontoidea; Tetraodontidae; Tetraodo
NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lutfalla G., Roest Crollius H., Stange-Thomas Mogensen K., Monneron D.; "Comparative genomic analysis reveals independences appecific gene family in vertebrates:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=99883;
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33.8%;
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; Pred. No. 1.86
41; Mismatches
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                                                                     Percomorpha;
Tetraodon.
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Euteleostei; Neoteleostei;
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Best Local 9
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01-OCT-2003
01-OCT-2003
01-MAR-2004
                                                                   HSSP; P13722; iJPS.
GO; GO:0016020; C:membrane; IEA,
GO; GO:00160496; F:hematopoietin/interferon-class
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR008957; FN_III-like.
                                       Receptor;
                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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Libmitted (FEB-2003) ...

MBL; AJ544911; CAD67769.1; -..

30; GG:0016020; C:membrane; IEA.

30; GG:0014896; F:hematopoletin/interferon-class (D:G0:G0:0004872; F:receptor activity; IEA.

InterPro; IPR000282; Cytok_receptor_2.

TOR0008957; FN_III-like.
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                                                                                                                                                                                               Genes Immun.
EMBL; AJ55548
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    SEQUENCE
                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley; TISSU
Weiss B., Wolk K., Gruenberg
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytokine receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=crf2-s1;
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                                                                                                                                                                                                                                                          "Cloning of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                               Immun. 5:330-336(2004).
AJ555485; CAD88475.1; -
                                                                                                                                                                                                                                    counterpart."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSASLESETSVFIASVNLRNVLEWTEGNDTPS-NATETVOYAIYGDSDKRRSVRWRALQR
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                                                       Signal
  229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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enberg B.H., Vo
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cytokine receptor family 5CFFD37652A99365 CRC64;
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Matches 74
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J. Chen J., Chow B., Chui C., Crowley C., Currell B., Dewel B., Dowd Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D Vandlen R., Yann J., Zhang M., Zhang Z., Goddard A., Wood W.I., Coloniti B., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                    GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoietin/interferon-class
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR000957; FN III-like.
SEQUENCE 262 AA; 30418 MW; E46EEF4DE78ADFDA C
                                                                                                                                                                                                                                                                                                                                                                                                       bioinformatics assessment.",
Genome Res. 13:2265-2270(2003).
EMBL; AY358737; AAQ89097.1; --
HSSP; P24055; 1A21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The secreted protein discovery initiative effort to identify novel human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski P.;
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                  GRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSN1KYNVSVL
                                                             FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT
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Primates;
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Last annotation updat
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Pred. No. 2.7e-20;
0; Mismatches 97
                                                                                                                                                                                                                                             Score 310; DB 2;
Pred. No. 9e-20;
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                                                                                                                                                                                                                          Mismatches
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Best Local
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Q969J5;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2004 (TrEMBLrel. 27, Last annotation update)
SOLUBLE cytokine class II receptor; long isoform pr
(Interleukin 22-binding protein CRF2-10L).
Name=CRF2-S1; Synonyms=IL22BP;
Heno sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kotenko S.V., Izotova I.S., Mirochnitchenko O.V., Esterova Dickensheets H., Donnelly R.P., Pestka S.; "Identification, cloning, and characterization of a novel receptor that binds IL-22 and neutralizes its activity."; J. Immunol. 166:7096-7103(2001).
EMBL; AJ313162; CAC85635.1; -.
EMBL; AY040567; AAK85715.1; -.
EMSP; P24055; 1A21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A novel, soluble homologue of the human preferential expression in placenta."; Genes Immun. 2:329-334(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:14901; IL22RA2.
GO; GO:0015020; C:membrane; IEA.
GO; GO:0004896; F:nematopoietin/interferon-class
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR008957; FN_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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MEDLINE=21286453; PubMed=11390454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21518574; PubMed=11607789; DOI=10.1038/sj
Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
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                                                                            PRETEWMETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFII
                                                                                                                                                        FPGCRTLAKYGORQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT
                                                                                                                                                                                                                                    KPQRVQFQSRNFHNILQWQPGRALTGNSSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVABIYQPMLDRRSQRSEERC
                                    NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPGPPRRAQPSEKQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                263 AA;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
                                                                                                                                                                                             -YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAES
                                                                                                                                                                                                                                                                                                                                                                                                                                     21
263
                                                                                                                                                                                                                                                                                                                                                                                                30550
                                                                                                                                                                                                                                                                                                                                    25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                  Score 310; DB 2;
Pred. No. 9.1e-20;
3; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                Potential. soluble cytokine class II isoform.
                                                                                                                                                                                                                                                                                                                                                                                                C96ECEC5D78AC79B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL-10 receptor with
                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                         Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (D200-domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .gene.6363786;
L., Kunz S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Esterova
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      soluble
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    259
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Best Local S
Matches 65
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Q7TNIS;
Q7TNIS;
01-OCT-2003 (TrEMBI
01-OCT-2003 (TrEMBI
01-MAR-2004 (TrEMBI
Putative cytokine;
                                                                                                                                                                                                                                                                            Q80XF5
Q80XF5;
Q1-JUN-2003
01-JUN-2003
01-MAR-2004
                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Interleukin 22 soluble receptor.
Name=Il22ra2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
SIGNAL
SEQUENCE FROM N.A.
STRAIN-BALB/c;
MEDLINE-22586333; PubMed-12700595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Balb/c; TISSUE-Spleen;
Weiss B., Wolk K., Gruenberg
                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=CRF2-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MBL; AJ555484; CAD88474.1; -.
SSP, P13726; 1JPS.
O; GO:0005829; C:cytosol; IDA.
O; GO:0005515; F:protein binding; IPI.
O; GO:0042516; P:regulation of tyrosine ph
nterPro; IPR000282; Cytok receptor_2.
nterro; IPR0008957; FN_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                             11
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65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAEMYOPMFDRRSPRSKERC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KWKRNPEDLPVSMQQIYSNLKYNVSVLNT---KSNRTWSQCVTNHTLVLTWLEPNTLYCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POKVRFOSRNFHNILHWQAGSSLPSNNSIYFVQYKMYGQSQWEDKVDCWGTTALFCDLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVESFVPGPPRRAQPSEKQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPNRNQSGKNASMETYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PANITFLSINMKNVLOWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCDLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5:330-336(2004).
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                                                                                                                                          Chordata;
Rodentia;
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230
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GLVYRVFTINNSLEKEQKAYEG--TQRAVEIEGLIPHSSYCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 277; DB 2;
Pred. No. 7.4e-17;
0; Mismatches 99
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soluble 1.
page 4EDFBAFC105
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                                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
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Sciurognathi; Muridae;
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y II soluble 1 precursor.
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     DOI=10.1038/sj.gene.6363947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                       Euteleostomi; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family
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PERMITT RESULT R
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Best Local S
Matches 64
               Genome Res. 9:242-250(1999).

EMBL; AF082667; AAD13678.1; -.

EMBL; AF082667; AAD13671.1; -.

EMBL; AF082665; AAD13671.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004896; F:hematopoietin/interferon-class (D

GO; GO:0004896; F:hematopoietin/interferon-class (D

GO; GO:0004876; F:hematopoietin/interferon-class (D

GO; GO:0004876; F:hematopoietin/interfero; IPR00282; Cytok receptor_2.

Interfero; IPR003961; FN_III-like.

Interfero; IPR003961; FN_III-like.

Interfero; IPR003957; FN_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9YGC8
Q9YGC8;
01-MAY-1999 (TrE
01-MAY-1999 (TrE
05-JUL-2004 (TrE
Interleukin-10 r
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Receptor.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                888
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[2]
                                                                                                                                                                                                                                                                                             Reboul J., Gardiner K.,
                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                     Reboul J., Gardiner K., Monneron "Comparative genomic analysis of
                                                                                                                                                                                                                                                                                                                   MEDLINE=99177346; PubMed=10077530;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang M.-S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALB/c
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"Cloning and
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GO:0005515;
GO:0042516;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                      gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPNRNQSGKNASMETYY-GLVYRVFTINNSLEKEQKAYEG--TQRAVEIEGLIPHSSYCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POKVRFOSRNFHNI LHWOAGSSLPSNNS I YFVOYKMYGOSOWEDKVDCWGTTALFCDLTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05829; C:cytosol; IDA.
05515; F:protein binding; IPI.
42516; P:regulation of tyrosine
IPR000282; Cytok receptor 2.
IPR008957; FN_III-like.
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Tissue
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2; Mismatches
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Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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use IL-22 binding protein.";
                                                                                                                                                                                                                                                                            Uze G., Lutfalla G.;
interferon/interleukin-10
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L.1e-16;
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XN [1]

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC TISSUE-Synovial membrane tissue;

RC TISSUE-Synovial membrane tissue;

RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Suzuki Y.,

RA Katsumoto K., Hirano M., Sano S., Momura R., Yoshikawa Y.,

RA Matsumoto K., Hirano M., Sano S., Momiyama H., Onogawa S.,

RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,

RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,

RA Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,

RA Watanabe M., Sugiyama T., Isono Y., Kawai-Hio Y., Sato H., Wakamatsu A.,

RA Kimura K., Yamamoto J., Isono Y., Kawai-Hio Y., Sato K., Nishikawa T.,

RA Kimura K., Yamamoto J., Isono Y., Kawai-Hio Y., Sekine M.,

RA Kikuchi H., Kanda K., Wagateuma M., Murakawa K., Kanehori K.,

RA Kikuchi H., Kanda K., Wagateuma M., Murakawa K., Kanehori K.,

RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

DR GO; GO:0016020; C:membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR CO:0004872; F:receptor activity; IEA.

T--~PPTO: IPR000282; Cytok_receptor_2.

T--~PPTO: IPR008957; FN_III-like.
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Q6ZVU9
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SEQUENCE
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05-JUL-2004 (TrEMBLrel. 27, La
05-JUL-2004 (TrEMBLrel. 27, La
05-JUL-2004 (TrEMBLrel. 27, La
Hypothetical protein FLJ42063.
Homo sapiens (Human)
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SMART; SM00060;
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CDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYFFLETQIGFPEVALITDEKSISVV
                                                                                     GMVPPPENVRMNSVNFKNILOWESPAFAEG-NLTFTAQYLSYR----IFQDKCMNTTLTE
                                                                                                                                            GGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTY
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Primates;
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Pred. No. 1.0
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Pred. No. 9.8e-13
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RESULT 14
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008334;
01-FEB-1995
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SEQUENCE FROM N.A.
MEDLINE=96054036; PubMed=7563119;
Lutfalla G., McInnis M.G., Antonarakis
Lutfalla G., frhe human CRFB4 gene: com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                    Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Sti

Wood W.I., Goddard A.D., Gurney A.L.;

"Interleukin (IL)-22, a novel human cytokine that signals

interferon receptor-related proteins CRF2-4 and IL-22R.";

J. Biol. Chem. 275:31335-31339 (2000)

-1-FUNCTION: Receptor for IL10 and IL22. Serves as an accu-

essential for the active IL10 receptor complex and to

IL10-induced signal transduction events.
                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=15340161; DOI=10.1110/ps.04682504; Zhang Z., Henzel W.J.; "Signal peptide prediction based on analy verified cleavage sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lutfalla G., McInnis M.C.
"Structure of the human neighbor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93300510; PubMed=8314576;
Lutfalla G., Gardiner K., Uze G.;
"A new member of the cytokine receptor
21 at less than 35 kb from IFNAR.";
Genomics 16:366-373(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-FEB-1995 (Rel. 31, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Interleukin-10 receptor beta chain precursor (IL
(Cytokine receptor family 2 member 4) (Cytokine
                                         -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the type II cytokine family o
-!- SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                   MEDLINE=20469498; PubMed=10875937; DOI=10.1074/jbc.M005304200;
Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson
                                                                                                                                                                                                                                                                                                                        MEDLINE=97459974; PubMed=9312047;
Kotenko S.V., Krause C.D., Izotova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 20-34.
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              This SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                           "Identification and functional characterization
                                                                                                                                                                                                                                                                                                           Pestka S.;
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) J. 16:5894-5903(1997).
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Swiss
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 Bioinformatics
                                                                                                                                                                                                                                                                                                                         DOI=10.1093/emboj/16.19
a L.S., Pollack B.P., Wu
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   It is produced through a collaboration informatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comparison with
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GO; GO:0016021; C:integ...

GO; GO:0001886; C:plasma membrane; IAS.

GO; GO:0004920; P:interleukin-10 receptor activity

GO; GO:0004920; P:receptor activity; TAS.

GO; GO:000695; P:immune response; TAS.

GO; GO:0006954; P:inflammatory response; TAS.

GO; GO:0007165; P:signal transduction; TAS.

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR000282; Cytok receptor_2.

InterPro; IPR0008957; FN_IIT-1ike.

InterPro; IPR0018957; FN_IIT-1ike.

InterPro; IPR0018957; FN_GO;

Pfam; P00108; Tissue factor.

R Pfam; P00108; Tissue fac; I.

R Pfam; P00108; Tissue fac; I.

R Direct protein sequencing; Glycoprotein; Receptor_3.
                 Q9BUU4;
Q9BUU4;
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01-JUN-2001
25-OCT-2004
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EMBL; U08988; AAA86872.1;
PIR; A47003; A47003.
HSSP; P13726; 1TFH.
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PLGHP -> VGRME (in Ref. 2).

Missing (in Ref. 2).

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Potential.
Cytoplasmic (Potential).
Fibronectin type-III.
By similarity.
By similarity.
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Pred. No. 1.2e-12;
6; Mismatches 94;
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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA S.S., Loquellano N.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., MoEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.B.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
Tennews C.M. Ra Radriguez A.C., Sheron M.A.,
Tennews C.M. Radriguez A.C., Sheron M.A.,
Tennews C.M. Radriguez B. R.M., Schein J.B.,
Tennews C.M. Radriguez A.C., Sheron M.C.,
Tennews C.M. Radriguez B.M.
                                                                                                                                     Matches
                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                   Phelan M., Farmer A., Submitted (AUG-2003) to the EMBL/ Submitted (AUG-2003) to the EMBL/ EMBL; BC001903; AAH01903.1; -. EMBL; AY323826; AAP72016.1; -. TWART: BT009777; AAP88779.1; -.
                                                                                                                                                                                                      Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                          InterPro; InterPro;
                                                                                                                                                                                                                                                                                                                                HSSP; P13726; ITFH.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain...

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007596; P:blood coagulation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Rieder M.J., Carrington
Ahearn M.O., Kuldanek S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
74
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                                                                                                                                     63;
                                                                                                                                                                                                                                          SM00060;
                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                      ); IPR000282; Cytok_recepto

); IPR003961; FN_III.

); IPR008957; FN_III-like.

); IPR001187; Tissue_factor

701108; Tissue_fac; I.
                           CDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVV
                                                               GMVPPPENVRMNSVNFKNILOWESPAFAKG-NLTFTAQYLSYR----IFQDKCMNTTLTE
                                                                                    GGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
CDFSSLSKYGDHT---LRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.A.;
(JUN-2003)
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                                                                                                                                     Conservative
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                                                                                                                                                                                                                                          FN3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
                                                                                                                                                     19.4%;
29.2%;
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.A., Rajkumar N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s A., Halleck A., Hines
Moreira D., Kelley T.,
                                                                                                                                   36;
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                                                                                                                                                                                                                                                                                                                       receptor_2.
                                                                                                                                   Score 232.5; Pred. No. 1.2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                            factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99:16899-16903 (2002)
                                                                                                                                                                                                        E470726619AF54C2 CRC64;
                                                                                                                                                   No. 1.2e-1
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h E.J., Yi
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                                                                                                                                     Indels
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aer J., Lin
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